

SEQUENCE LISTING

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<110> Wonderling, Ramani S.
      Boroughs, Karen L.

<120> CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES
      THEREOF

<130> IM-5

<140> 09/917,265
<141> 2001-07-27

<150> 60/223,016
<151> 2000-08-04

<160> 111

<170> PatentIn version 3.2

<210> 1
<211> 514
<212> DNA
<213> Felis catus

<220>
<221> CDS
<222> (114)..(512)

<220>
<221> misc_feature
<222> (470)..(470)
<223> n = unknown at position 470
Xaa = unknown at position 119

<400> 1
gctaaaggcg ctcttgccac cttctgccat ctacacagct caggaaaaga aaggggacctc      60
aaaccttcca gatcccttcc tctcttagga aactattgag cacagggata aag atg      116
                                     Met
                                     1

act gct ata cca gta gat gat tgc atc aac ttt gtg gga atg aaa ttt      164
Thr Ala Ile Pro Val Asp Asp Cys Ile Asn Phe Val Gly Met Lys Phe
          5                      10                      15

att gac aat aca ctt tac ttt gta gct gac agt gat gaa aac ctg gaa      212
Ile Asp Asn Thr Leu Tyr Phe Val Ala Asp Ser Asp Glu Asn Leu Glu
          20                      25                      30

aca gat tac ttt ggc aag ctt gaa cat aaa ctc tca atc tta cga aac      260
Thr Asp Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn
          35                      40                      45

ttg aac gac caa gtt ctc ttc att aac cag gga gat caa cct gtg ttt      308
Leu Asn Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe

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50	55	60	65	
gag gat atg cct gat tct gac tgt aca gat aat gca ccc cgg act gaa				356
Glu Asp Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr Glu				
	70	75	80	
ttt atc ata tat atg tat aaa gat agc ctc act aga ggt ctg gca gta				404
Phe Ile Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val				
	85	90	95	
acc atc tct gtg aat tat aag acc atg tct act ctc tcc tgt gag aac				452
Thr Ile Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn				
	100	105	110	
aaa att att tcc ttt aan gga atg agt cct cct gag agt atc aat gat				500
Lys Ile Ile Ser Phe Xaa Gly Met Ser Pro Pro Glu Ser Ile Asn Asp				
	115	120	125	
gaa gga aat gac at				514
Glu Gly Asn Asp				
130				

<210> 2
 <211> 133
 <212> PRT
 <213> Felis catus

 <220>
 <221> misc_feature
 <222> (119)..(119)
 <223> The 'Xaa' at location 119 stands for Lys, or Asn.

 <400> 2

Met Thr Ala Ile Pro Val Asp Asp Cys Ile Asn Phe Val Gly Met Lys				
1	5	10	15	
Phe Ile Asp Asn Thr Leu Tyr Phe Val Ala Asp Ser Asp Glu Asn Leu				
	20	25	30	
Glu Thr Asp Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg				
	35	40	45	
Asn Leu Asn Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val				
	50	55	60	
Phe Glu Asp Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr				
65	70	75	80	
Glu Phe Ile Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala				
	85	90	95	

Val Thr Ile Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu
 100 105 110

Asn Lys Ile Ile Ser Phe Xaa Gly Met Ser Pro Pro Glu Ser Ile Asn
 115 120 125

Asp Glu Gly Asn Asp
 130

<210> 3
 <211> 514
 <212> DNA
 <213> Felis catus

<220>
 <221> misc_feature
 <222> (45)..(45)
 <223> n = unknown at position 45

<400> 3
 atgtcatttc cttcatcatt gatactctca ggaggactca ttcnttaaa ggaaataatt 60
 ttgtttctcac aggagagagt agacatgggc ttataattca cagagatggg tactgccaga 120
 cctctagtga ggctatcttt atacatatat atgataaatt cagtccgggg tgcattatct 180
 gtacagtcag aatcagggcat atcctcaaac acaggttgat ctccctgggt aatgaagaga 240
 acttggtcgt tcaagtttcg taagattgag agtttatggt caagcttgcc aaagtaatct 300
 gtttccaggt tttcatcact gtcagctaca aagtaaagtg tattgtcaat aaatttcatt 360
 cccacaaagt tgatgcaatc atctactggg atagcagtc tctttatccc tgtgctcaat 420
 agtttcctaa gagaggaagg gatctggaag gtttgaggtc cctttctttt cctgagctgt 480
 gtagatggca gaaggtggca ggagcgcctt tagc 514

<210> 4
 <211> 502
 <212> DNA
 <213> Felis catus

<220>
 <221> CDS
 <222> (3)..(464)
 <220>
 <221> misc_feature

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<222> (126)..(126)
<223> n = unknown at position 126
Xaa = unknown at position 42

<400> 4
gc aag ctt gaa cat aaa ctc tca atc tta cga aac ttg aac gac caa      47
  Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn Leu Asn Asp Gln
    1             5             10             15

gtt ctc ttc att aac cag gga gat caa cct gtg ttt gag gat atg cct      95
Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe Glu Asp Met Pro
    20             25             30

gat tct gac tgt aca gat aat gca ccc cgg nct gaa ttt atc ata tat      143
Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Xaa Glu Phe Ile Ile Tyr
    35             40             45

atg tat aaa gat agc ctc act aga ggt ctg gca gta acc atc tct gtg      191
Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val Thr Ile Ser Val
    50             55             60

aat tat aag acc atg tct act ctc tcc tgt gag aac aaa att att tcc      239
Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn Lys Ile Ile Ser
    65             70             75

ttt aag gaa atg agt cct cct gag agt atc aat gat gaa gga aat gac      287
Phe Lys Glu Met Ser Pro Pro Glu Ser Ile Asn Asp Glu Gly Asn Asp
    80             85             90             95

atc ata ttc ttt cag aga agt gtt cca gga cat gat gat aag ata caa      335
Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asp Lys Ile Gln
    100            105            110

ttt gag tct tca ttg tac aag ggg tac ttt cta gct tgt gaa aaa gag      383
Phe Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu Lys Glu
    115            120            125

aaa gat ctt ttc aaa ctc att ttg aaa aaa aag gat gaa aat ggg gat      431
Lys Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp
    130            135            140

aag tcc ata atg ttc act gtt caa aac aag aat tagatattaa aattgcataa      484
Lys Ser Ile Met Phe Thr Val Gln Asn Lys Asn
    145            150

tttgaaaaaa aaaaaaaa      502

<210> 5
<211> 154
<212> PRT
<213> Felis catus

<220>
<221> misc_feature
<222> (42)..(42)
<223> The 'Xaa' at location 42 stands for Thr, Ala, Pro, or Ser.

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<400> 5

Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn Leu Asn Asp Gln Val
1 5 10 15

Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe Glu Asp Met Pro Asp
20 25 30

Ser Asp Cys Thr Asp Asn Ala Pro Arg Xaa Glu Phe Ile Ile Tyr Met
35 40 45

Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val Thr Ile Ser Val Asn
50 55 60

Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn Lys Ile Ile Ser Phe
65 70 75 80

Lys Glu Met Ser Pro Pro Glu Ser Ile Asn Asp Glu Gly Asn Asp Ile
85 90 95

Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asp Lys Ile Gln Phe
100 105 110

Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu Lys Glu Lys
115 120 125

Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp Lys
130 135 140

Ser Ile Met Phe Thr Val Gln Asn Lys Asn
145 150

<210> 6

<211> 502

<212> DNA

<213> Felis catus

<220>

<221> misc_feature

<222> (377)..(377)

<223> n = unknown at position 377

<400> 6

tttttttttt ttttcaaatt atgcaatttt aatatctaatt tcttgttttg aacagtgaac 60

attatggact tatccccatt ttcattccttt tttttcaaaa tgagtttgaa aagatctttc	120
tctttttcac aagctagaaa gtacccttg tacaatgaag actcaaattg tatcttatca	180
tcatgtcctg gaacacttct ctgaaagaat atgatgtcat ttccttcac attgatactc	240
tcaggaggac tcatttcctt aaaggaaata attttggttct cacaggagag agtagacatg	300
gtcttataat tcacagagat gggtactgcc agacctctag tgaggctatc tttatacata	360
tatatgataa attcagnccg ggggtgcatta tctgtacagt cagaatcagg catatcctca	420
aacacaggtt gatctccctg gttaatgaag agaacttggc cgttcaagtt tcgtaagatt	480
gagagtttat gttcaagctt gc	502

<210> 7
 <211> 607
 <212> DNA
 <213> Felis catus

<220>
 <221> CDS
 <222> (24)..(599)

<400> 7 aactattgag cacagggata aag atg act gct ata cca gta gat gat tgc atc <div style="text-align: center;"> Met Thr Ala Ile Pro Val Asp Asp Cys Ile 1 5 10 </div>	53
aac ttt gtg gga atg aaa ttt att gac aat aca ctt tac ttt gta gct Asn Phe Val Gly Met Lys Phe Ile Asp Asn Thr Leu Tyr Phe Val Ala <div style="text-align: center;"> 15 20 25 </div>	101
gac agt gat gaa aac ctg gaa aca gat tac ttt ggc aag ctt gaa cat Asp Ser Asp Glu Asn Leu Glu Thr Asp Tyr Phe Gly Lys Leu Glu His <div style="text-align: center;"> 30 35 40 </div>	149
aaa ctc tca atc tta cga aac ttg aac gac caa gtt ctc ttc att aac Lys Leu Ser Ile Leu Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asn <div style="text-align: center;"> 45 50 55 </div>	197
cag gga gat caa cct gtg ttt gag gat atg cct gat tct gac tgt aca Gln Gly Asp Gln Pro Val Phe Glu Asp Met Pro Asp Ser Asp Cys Thr <div style="text-align: center;"> 60 65 70 </div>	245
gat aat gca ccc cgg act gaa ttt atc ata tat atg tat aaa gat agc Asp Asn Ala Pro Arg Thr Glu Phe Ile Ile Tyr Met Tyr Lys Asp Ser <div style="text-align: center;"> 75 80 85 90 </div>	293
ctc act aga ggt ctg gca gta acc atc tct gtg aat tat aag acc atg Leu Thr Arg Gly Leu Ala Val Thr Ile Ser Val Asn Tyr Lys Thr Met <div style="text-align: center;"> 95 100 105 </div>	341
tct act ctc tcc tgt gag aac aaa att att tcc ttt aag gaa atg agt	389

Ser Thr Leu Ser Cys Glu Asn Lys Ile Ile Ser Phe Lys Glu Met Ser
 110 115 120
 cct cct gag agt atc aat gat gaa gga aat gac atc ata ttc ttt cag 437
 Pro Pro Glu Ser Ile Asn Asp Glu Gly Asn Asp Ile Ile Phe Phe Gln
 125 130 135
 aga agt gtt cca gga cat gat gat aag ata caa ttt gag tct tca ttg 485
 Arg Ser Val Pro Gly His Asp Asp Lys Ile Gln Phe Glu Ser Ser Leu
 140 145 150
 tac aag ggg tac ttt cta gct tgt gaa aaa gag aaa gat ctt ttc aaa 533
 Tyr Lys Gly Tyr Phe Leu Ala Cys Glu Lys Glu Lys Asp Leu Phe Lys
 155 160 165 170
 ctc att ttg aaa aaa aag gat gaa aat ggg gat aag tcc ata atg ttc 581
 Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp Lys Ser Ile Met Phe
 175 180 185
 act gtt caa aac aag aat tagatatt 607
 Thr Val Gln Asn Lys Asn
 190
 <210> 8
 <211> 192
 <212> PRT
 <213> Felis catus
 <400> 8
 Met Thr Ala Ile Pro Val Asp Asp Cys Ile Asn Phe Val Gly Met Lys
 1 5 10 15
 Phe Ile Asp Asn Thr Leu Tyr Phe Val Ala Asp Ser Asp Glu Asn Leu
 20 25 30
 Glu Thr Asp Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg
 35 40 45
 Asn Leu Asn Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val
 50 55 60
 Phe Glu Asp Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr
 65 70 75 80
 Glu Phe Ile Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala
 85 90 95
 Val Thr Ile Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu
 100 105 110

Asn Lys Ile Ile Ser Phe Lys Glu Met Ser Pro Pro Glu Ser Ile Asn
 115 120 125

Asp Glu Gly Asn Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His
 130 135 140

Asp Asp Lys Ile Gln Phe Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu
 145 150 155 160

Ala Cys Glu Lys Glu Lys Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys
 165 170 175

Asp Glu Asn Gly Asp Lys Ser Ile Met Phe Thr Val Gln Asn Lys Asn
 180 185 190

<210> 9
 <211> 576
 <212> DNA
 <213> Felis catus

<400> 9
 atgactgcta taccagtaga tgattgcac aactttgtgg gaatgaaatt tattgacaat 60
 acactttact ttgtagctga cagtgatgaa aacctggaaa cagattactt tggcaagctt 120
 gaacataaac tctcaatctt acgaaacttg aacgaccaag ttctcttcat taaccaggga 180
 gatcaacctg tgtttgagga tatgcctgat tctgactgta cagataatgc accccggact 240
 gaatttatca tatatatgta taaagatagc ctactagag gtctggcagt aaccatctct 300
 gtgaattata agaccatgtc tactctctcc tgtgagaaca aaattatttc ctttaaggaa 360
 atgagtcctc ctgagagtat caatgatgaa ggaaatgaca tcatattctt tcagagaagt 420
 gttccaggac atgatgataa gatacaattt gagtcttcat tgtacaaggg gtactttcta 480
 gcttgtgaaa aagagaaaga tcttttcaaa ctcatatttga aaaaaaagga tgaaaatggg 540
 gataagtcca taatgttcac tgttcaaaac aagaat 576

<210> 10
 <211> 607
 <212> DNA
 <213> Felis catus

<400> 10
 aatatcta tcttggtttg aacagtgaac attatggact tatccccatt ttcacatctt 60


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tttttcaaaa tgagtttgaa aagatctttc tctttttcac aagctagaaa gtacccttg 120
tacaatgaag actcaaattg tatcttatca tcatgtcctg gaacacttct ctgaaagaat 180
atgatgtcat ttccttcac attgatactc tcaggaggac tcatttcctt aaaggaaata 240
attttgttct cacaggagag agtagacatg gtcttataat tcacagagat gggttactgcc 300
agacctctag tgaggctatc tttatacata tatatgataa attcagtcctg ggggtgcatta 360
tctgtacagt cagaatcagg catatcctca aacacagggt gatctccctg gttaatgaag 420
agaacttggg cgttcaagtt tcgtaagatt gagagtttat gttcaagctt gccaaagtaa 480
tctgtttcca ggttttcac actgtcagct acaaagtaaa gtgtattgtc aataaatttc 540
attcccacaa agttgatgca atcatctact ggtatagcag tcattcttat cctgtgtctc 600
aatagtt 607

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<210> 11
<211> 471
<212> DNA
<213> Felis catus

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<220>
<221> CDS
<222> (1)..(471)

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Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn Leu Asn
1 5 10 15

gac caa gtt ctc ttc att aac cag gga gat caa cct gtg ttt gag gat 96
Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe Glu Asp
20 25 30

atg cct gat tct gac tgt aca gat aat gca ccc cgg act gaa ttt atc 144
Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr Glu Phe Ile
35 40 45

ata tat atg tat aaa gat agc ctc act aga ggt ctg gca gta acc atc 192
Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val Thr Ile
50 55 60

tct gtg aat tat aag acc atg tct act ctc tcc tgt gag aac aaa att 240
Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn Lys Ile
65 70 75 80

att tcc ttt aag gaa atg agt cct cct gag agt atc aat gat gaa gga 288
Ile Ser Phe Lys Glu Met Ser Pro Pro Glu Ser Ile Asn Asp Glu Gly
85 90 95

aat gac atc ata ttc ttt cag aga agt gtt cca gga cat gat gat aag 336

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Asn Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asp Lys
100 105 110

ata caa ttt gag tct tca ttg tac aag ggg tac ttt cta gct tgt gaa 384
Ile Gln Phe Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu
115 120 125

aaa gag aaa gat ctt ttc aaa ctc att ttg aaa aaa aag gat gaa aat 432
Lys Glu Lys Lys Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn
130 135 140

ggg gat aag tcc ata atg ttc act gtt caa aac aag aat 471
Gly Asp Lys Ser Ile Met Phe Thr Val Gln Asn Lys Asn
145 150 155

<210> 12
<211> 157
<212> PRT
<213> Felis catus

<400> 12

Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn Leu Asn
1 5 10 15

Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe Glu Asp
20 25 30

Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr Glu Phe Ile
35 40 45

Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val Thr Ile
50 55 60

Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn Lys Ile
65 70 75 80

Ile Ser Phe Lys Glu Met Ser Pro Pro Glu Ser Ile Asn Asp Glu Gly
85 90 95

Asn Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asp Lys
100 105 110

Ile Gln Phe Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu
115 120 125

Lys Glu Lys Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn
130 135 140

Gly Asp Lys Ser Ile Met Phe Thr Val Gln Asn Lys Asn
 145 150 155

<210> 13
 <211> 471
 <212> DNA
 <213> Felis catus

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 aatgagtttg aaaagatctt tctctttttc acaagctaga aagtaccctt tgtacaatga 120
 agactcaa at tgtatcttat catcatgtcc tggaacactt ctctgaaaga atatgatgtc 180
 atttccttca tcattgatac tctcaggagg actcatttcc ttaaaggaaa taattttggtt 240
 ctcacaggag agagtagaca tgggtcttata attcacagag atgggtactg ccagacctct 300
 agtgaggcta tctttataca tatatatgat aaattcagtc cgggggtgcat tatctgtaca 360
 gtcagaatca ggcatactct caaacacagg ttgatctccc tgggttaatga agagaacttg 420
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<210> 14
 <211> 1233
 <212> DNA
 <213> Felis catus

<220>
 <221> CDS
 <222> (1)..(1230)

<400> 14
 atg gcc gac aag gtc ctg aag gag aag agg aag cag ttc atc aac tca 48
 Met Ala Asp Lys Val Leu Lys Glu Lys Arg Lys Gln Phe Ile Asn Ser
 1 5 10 15
 gtc ggc atg ggg acg gtc aac ggc ttg ctg gat gaa ctc ttt gag aaa 96
 Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp Glu Leu Phe Glu Lys
 20 25 30
 aac gtg ctg aac cag gag gag atg gag aga gta aaa tgt gaa aac gct 144
 Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val Lys Cys Glu Asn Ala
 35 40 45
 acc gtt atg gac aag gcc cga gct ctg atc gac agc gtc ctg cgg aaa 192
 Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp Ser Val Leu Arg Lys
 50 55 60
 ggg cca cgg gcg tgc cag atc ttt atc tgt cac atc tgt gag gaa gac 240

Gly 65	Pro	Arg	Ala	Cys	Gln 70	Ile	Phe	Ile	Cys	His 75	Ile	Cys	Glu	Glu	Asp 80	
acc	cac	ctt	gca	gag	acg	ctg	ggg	ctc	tcc	tca	agc	cca	caa	tct	gga	288
Thr	His	Leu	Ala	Glu 85	Thr	Leu	Gly	Leu	Ser 90	Ser	Ser	Pro	Gln	Ser 95	Gly	
aat	tct	cag	aac	acc	acg	gac	tct	gaa	gta	gcg	ttt	cct	cct	ctt	cca	336
Asn	Ser	Gln	Asn 100	Thr	Thr	Asp	Ser	Glu 105	Val	Ala	Phe	Pro	Pro 110	Leu	Pro	
gcc	agc	gtg	aat	aac	atg	cct	ggg	ccg	gct	gag	cca	gaa	gaa	tct	gta	384
Ala	Ser	Val 115	Asn	Asn	Met	Pro	Gly 120	Pro	Ala	Glu	Pro	Glu 125	Glu	Ser	Val	
gat	gct	ctc	aag	ctt	tgt	cct	cgt	gaa	aac	ttc	gtg	aaa	ctg	tgt	aaa	432
Asp	Ala	Leu	Lys	Leu	Cys	Pro	Arg 135	Glu	Asn	Phe	Val 140	Lys	Leu	Cys	Lys	
cag	agg	gct	gaa	gag	atc	tac	cca	ata	aag	gag	aga	aag	gat	cgt	act	480
Gln	Arg	Ala	Glu	Glu	Ile 150	Tyr	Pro	Ile	Lys	Glu 155	Arg	Lys	Asp	Arg 160	Thr	
cgt	ctg	gct	ctc	atc	ata	tgc	aat	acg	acg	ttc	gat	cat	ctt	tct	ctc	528
Arg	Leu	Ala	Leu	Ile 165	Ile	Cys	Asn	Thr 170	Thr	Phe	Asp	His	Leu	Ser 175	Leu	
agg	aag	ggg	gct	gac	ctt	gac	gtt	gca	ggg	atg	agg	agg	ctg	ctt	aca	576
Arg	Lys	Gly	Ala	Asp 180	Leu	Asp	Val	Ala 185	Gly	Met	Arg	Arg	Leu 190	Leu	Thr	
gac	ctt	ggc	tac	agt	gtg	cac	ata	aaa	gag	gaa	ctc	act	gct	aag	gac	624
Asp	Leu	Gly	Tyr	Ser	Val	His	Ile 200	Lys	Glu	Glu	Leu	Thr 205	Ala	Lys	Asp	
atg	gaa	tca	gag	ctg	agg	gca	ttt	gct	gcc	cgt	cca	gag	cac	aag	tcc	672
Met	Glu	Ser	Glu	Leu	Arg	Ala 215	Phe	Ala	Ala	Arg	Pro 220	Glu	His	Lys	Ser	
tcg	gac	agc	aca	ttc	ctg	gtg	ttc	atg	tct	cat	ggc	atc	ctg	agt	gga	720
Ser	Asp	Ser	Thr	Phe	Leu	Val 230	Phe	Met	Ser	His 235	Gly	Ile	Leu	Ser 240	Gly	
atc	tgt	ggg	acg	aag	tac	agc	gct	gaa	gga	gac	cca	gat	gta	ttg	gct	768
Ile	Cys	Gly	Thr	Lys 245	Tyr	Ser	Ala	Glu	Gly	Asp 250	Pro	Asp	Val	Leu 255	Ala	
tat	gac	acc	atc	ttc	cag	att	ttc	aac	aac	cgc	aac	tgc	ctt	agt	cta	816
Tyr	Asp	Thr	Ile	Phe 260	Gln	Ile	Phe	Asn 265	Asn	Arg	Asn	Cys	Leu 270	Ser	Leu	
aag	gac	aag	ccc	aag	gtc	atc	atc	gtc	cag	gcc	tgc	aga	ggg	gaa	aat	864
Lys	Asp	Lys	Pro	Lys 275	Val	Ile	Ile	Val 280	Gln	Ala	Cys	Arg 285	Gly	Glu	Asn	
ttg	ggg	gaa	ctg	ttg	atc	agt	gac	tct	cca	gcg	gcc	cca	atg	gac	agc	912
Leu	Gly	Glu	Leu	Leu	Ile	Ser	Asp	Ser	Pro	Ala	Ala	Pro	Met	Asp	Ser	

290	295	300	
act tca cag atg ggt agc agc ctt tca cag gtg ggt gac aac cta gag			960
Thr Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu			
305	310	315	320
gac gac gcc att tac aag gtc cac gtg gag aag gac ttc atc gct ttc			1008
Asp Asp Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe			
	325	330	335
tgc tcc tcg acc cca cat cat gtg tct tgg aga gac gtg aac aag gga			1056
Cys Ser Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly			
	340	345	350
tct ctc ttc att aca caa ctc atc acg tgc ttc caa aag tat tcg tgg			1104
Ser Leu Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp			
	355	360	365
tgc ttt cat ctg gag gaa gta ttt cgg aag gta caa cag tca ttt gaa			1152
Cys Phe His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu			
	370	375	380
aaa cca aat gtt aga gcc cag atg ccc acc att gaa cga cta tcc atg			1200
Lys Pro Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met			
385	390	395	400
aca aga tgt ttc tac ctc ttc cca gga cat taa			1233
Thr Arg Cys Phe Tyr Leu Phe Pro Gly His			
	405	410	
<210> 15			
<211> 410			
<212> PRT			
<213> Felis catus			
<400> 15			
Met Ala Asp Lys Val Leu Lys Glu Lys Arg Lys Gln Phe Ile Asn Ser			
1	5	10	15
Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp Glu Leu Phe Glu Lys			
	20	25	30
Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val Lys Cys Glu Asn Ala			
	35	40	45
Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp Ser Val Leu Arg Lys			
	50	55	60
Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His Ile Cys Glu Glu Asp			
65	70	75	80

Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser Ser Pro Gln Ser Gly
 85 90 95

Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala Phe Pro Pro Leu Pro
 100 105 110

Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu Pro Glu Glu Ser Val
 115 120 125

Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe Val Lys Leu Cys Lys
 130 135 140

Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu Arg Lys Asp Arg Thr
 145 150 155 160

Arg Leu Ala Leu Ile Ile Cys Asn Thr Thr Phe Asp His Leu Ser Leu
 165 170 175

Arg Lys Gly Ala Asp Leu Asp Val Ala Gly Met Arg Arg Leu Leu Thr
 180 185 190

Asp Leu Gly Tyr Ser Val His Ile Lys Glu Glu Leu Thr Ala Lys Asp
 195 200 205

Met Glu Ser Glu Leu Arg Ala Phe Ala Ala Arg Pro Glu His Lys Ser
 210 215 220

Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Gly Ile Leu Ser Gly
 225 230 235 240

Ile Cys Gly Thr Lys Tyr Ser Ala Glu Gly Asp Pro Asp Val Leu Ala
 245 250 255

Tyr Asp Thr Ile Phe Gln Ile Phe Asn Asn Arg Asn Cys Leu Ser Leu
 260 265 270

Lys Asp Lys Pro Lys Val Ile Ile Val Gln Ala Cys Arg Gly Glu Asn
 275 280 285

Leu Gly Glu Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser
 290 295 300

Thr Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu
 305 310 315 320

Asp Asp Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe
 325 330 335

Cys Ser Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly
 340 345 350

Ser Leu Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp
 355 360 365

Cys Phe His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu
 370 375 380

Lys Pro Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met
 385 390 395 400

Thr Arg Cys Phe Tyr Leu Phe Pro Gly His
 405 410

<210> 16
 <211> 1233
 <212> DNA
 <213> Felis catus

<400> 16
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 ctgggctcta acatttggtt tttcaaata ctgttgtacc ttccgaaata cttcctccag 120
 atgaaagcac cacgaatact tttggaagca cgtgatgagt tgtgtaatga agagagatcc 180
 cttgttcacg tctctccaag acacatgatg tggggctcag gagcagaaag cgatgaagtc 240
 cttctccacg tggaccttgt aaatggcgct gtcctctagg ttgtcaccca cctgtgaaag 300
 gctgctaccc atctgtgaag tgctgtccat tggggccgct ggagagtcac tgatcaacag 360
 ttccccaaa ttttcacctc tgcaggcctg gacgatgatg accttgggct tgtcctttag 420
 actaaggcag ttgcggttgt tgaaaatctg gaagatgggtg tcataagcca atacatctgg 480
 gtctccttca gcgctgtact tcgtcccaca gattccactc aggatgccat gagacatgaa 540
 caccaggaat gtgctgtccg aggacttggt ctctggacgg gcagcaaag ccctcagctc 600
 tgattccatg tccttagcag tgagttcctc ttttatgtgc aactgtagc caaggtctgt 660
 aagcagctc ctcacccctg caacgtcaag gtcagcccc ttctgagag aaagatgatc 720

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gaacgtcgta ttgcatatga tgagagccag acgagtacga tcctttctct cctttattgg      780
gtagatctct tcagccctct gtttacacag tttcacgaag ttttcacgag gacaaagctt      840
gagagcatct acagattctt ctggctcagc cggcccaggc atgttattca cgctggctgg      900
aagaggagga aacgctactt cagagtcctg ggtgttctga gaatttccag attgtgggct      960
tgaggagagc cccagcgtct ctgcaagggtg ggtgtcttcc tcacagatgt gacagataaa    1020
gatctggcac gcccgtaggc ctttccgcag gacgctgtcg atcagagctc gggccttgtc     1080
cataacggta gcgttttcac attttactct ctccatctcc tcttggttca gcacgttttt     1140
ctcaaagagt tcattccagca agccgttgac cgtcccatg cggactgagt tgatgaactg     1200
cttcctcttc tccttcagga ccttgtcggc cat                                  1233

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<210> 17
<211> 526
<212> DNA
<213> Felis catus

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<220>
<221> CDS
<222> (18)..(524)

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           Met Ala Asp Lys Asp Leu Lys Gly Lys Arg Lys
           1             5             10

cag ttc atc aac tca gtc ggc atg ggg acg gtc aac ggc ttg ctg gat      98
Gln Phe Ile Asn Ser Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp
           15             20             25

gaa ctc ttt gag aaa aac gtg ctg aac cag gag gag atg gag aga gta      146
Glu Leu Phe Glu Lys Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val
           30             35             40

aaa tgt gaa aac gct acc gtt atg gac aag gcc cga gct ctg atc gac      194
Lys Cys Glu Asn Ala Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp
           45             50             55

agc gtc ctg cgg aaa ggg cca cgg gcg tgc cag atc ttt atc tgt cac      242
Ser Val Leu Arg Lys Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His
           60             65             70             75

atc tgt gag gaa gac acc cac ctt gca gag acg ctg ggg ctc tcc tca      290
Ile Cys Glu Glu Asp Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser
           80             85             90

agc cca caa tct gga aat tct cag aac acc acg gac tct gaa gta gcg      338
Ser Pro Gln Ser Gly Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala

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	95	100	105	
ttt cct cct ctt cca gcc agc gtg aat aac atg cct ggg ccg gct gag				386
Phe Pro Pro Leu Pro Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu				
	110	115	120	
cca gaa gaa tct gta gat gct ctc aag ctt tgt cct cgt gaa aac ttc				434
Pro Glu Glu Ser Val Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe				
	125	130	135	
gtg aaa ctg tgt aaa cag agg gct gaa gag atc tac cca ata aag gag				482
Val Lys Leu Cys Lys Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu				
	140	145	150	155
aga aag gat cgt act cgt ctg gct ctc atc ata tgc aat acg ac				526
Arg Lys Asp Arg Thr Arg Leu Ala Leu Ile Ile Cys Asn Thr				
	160	165		

<210> 18
 <211> 169
 <212> PRT
 <213> Felis catus

<400> 18

Met Ala Asp Lys Asp Leu Lys Gly Lys Arg Lys Gln Phe Ile Asn Ser
1 5 10 15

Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp Glu Leu Phe Glu Lys
20 25 30

Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val Lys Cys Glu Asn Ala
35 40 45

Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp Ser Val Leu Arg Lys
50 55 60

Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His Ile Cys Glu Glu Asp
65 70 75 80

Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser Ser Pro Gln Ser Gly
85 90 95

Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala Phe Pro Pro Leu Pro
100 105 110

Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu Pro Glu Glu Ser Val
115 120 125

Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe Val Lys Leu Cys Lys
 130 135 140

Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu Arg Lys Asp Arg Thr
 145 150 155 160

Arg Leu Ala Leu Ile Ile Cys Asn Thr
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<210> 19
 <211> 526
 <212> DNA
 <213> Felis catus

<400> 19
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 gcatctacag attcttctgg ctacagccggc ccaggcatgt tattcacgct ggctggaaga 180
 ggaggaaacg ctacttcaga gtccgtggtg ttctgagaat ttccagattg tgggcttgag 240
 gagagcccca gcgtctctgc aagggtgggtg tcttcctcac agatgtgaca gataaagatc 300
 tggcacgccc gtggcccttt ccgcaggacg ctgtcgatca gagctcgggc cttgtccata 360
 acggtagcgt ttccacattt tactctctcc atctcctcct gggttcagcac gtttttctca 420
 aagagttcat ccagcaagcc gttgaccgtc cccatgccga ctgagttgat gaactgcttc 480
 ctcttgccct tcagatcctt gtcggccatg gctttttgct cgtgcc 526

<210> 20
 <211> 500
 <212> DNA
 <213> Felis catus

<220>
 <221> CDS
 <222> (3)..(362)

<220>
 <221> misc_feature
 <222> (473)..(473)
 <223> n = unknown at position 473

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 1 5 10 15

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Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu Asp	
20 25 30	
gac gcc att tac aag gtc cac gtg gag aag gac ttc atc gct ttc tgc	143
Asp Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe Cys	
35 40 45	
tcc tcg acc cca cat cat gtg tct tgg aga gac gtg aac aag gga tct	191
Ser Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly Ser	
50 55 60	
ctc ttc att aca caa ctc atc acg tgc ttc caa aag tat tcg tgg tgc	239
Leu Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp Cys	
65 70 75	
ttt cat ctg gag gaa gta ttt cgg aag gta caa cag tca ttt gaa aaa	287
Phe His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu Lys	
80 85 90 95	
cca aat gtt aga gcc cag atg ccc acc att gaa cga cta tcc atg aca	335
Pro Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met Thr	
100 105 110	
aga tac ttc tat ctc ttc cct ggc aat tgaaaatagc aatcatgggc	382
Arg Tyr Phe Tyr Leu Phe Pro Gly Asn	
115 120	
agtccagccc ttcttgacca acttggaata gtaccttagc tagcacaaca cactcattta	442
acgttttggtat tctcaataaaa aatgaaaaca nctaaaaaaa aaaaaaaaaa aaaaaaaaaa	500

<210> 21
 <211> 120
 <212> PRT
 <213> Felis catus

<400> 21

Glu Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser Thr Ser	
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Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu Asp Asp	
20 25 30	
Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe Cys Ser	
35 40 45	
Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly Ser Leu	
50 55 60	

Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp Cys Phe
65 70 75 80

His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu Lys Pro
85 90 95

Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met Thr Arg
100 105 110

Tyr Phe Tyr Leu Phe Pro Gly Asn
115 120

<210> 22
<211> 500
<212> DNA
<213> Felis catus

<220>
<221> misc_feature
<222> (28)..(28)
<223> n = unknown at position 28

<400> 22
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aatgagtgtg ttgtgctagc taaggctactt ttccaagttg gtcaagaagg gctggactgc 120
ccatgattgc tattttcaat tgccagggaa gagatagaag tatcttgtca tggatagtcg 180
ttcaatggtg ggcactctggg ctctaacatt tggtttttca aatgactggt gtaccttccg 240
aaatacttcc tccagatgaa agcaccacga atacttttgg aagcacgtga tgagtttgtt 300
aatgaagaga gatcccttgt tcacgtctct ccaagacaca tgatgtgggg tcgaggagca 360
gaaagcgatg aagtccttct ccacgtggac cttgtaaatg gcgtcgtcct ctaggttgtc 420
acccacctgt gaaaggctgc tacccatctg tgaagtgtg tccattgggg ccgctggaga 480
gtcactgatc aacagttccc 500

<210> 23
<211> 1230
<212> DNA
<213> Felis catus

<220>
<221> CDS
<222> (1)..(1230)

<400> 23

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Met Ala Asp Lys Asp Leu Lys Gly Lys Arg Lys Gln Phe Ile Asn Ser	
1 5 10 15	
gtc ggc atg ggg acg gtc aac ggc ttg ctg gat gaa ctc ttt gag aaa	96
Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp Glu Leu Phe Glu Lys	
20 25 30	
aac gtg ctg aac cag gag gag atg gag aga gta aaa tgt gaa aac gct	144
Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val Lys Cys Glu Asn Ala	
35 40 45	
acc gtt atg gac aag gcc cga gct ctg atc gac agc gtc ctg cgg aaa	192
Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp Ser Val Leu Arg Lys	
50 55 60	
ggg cca cgg gcg tgc cag atc ttt atc tgt cac atc tgt gag gaa gac	240
Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His Ile Cys Glu Glu Asp	
65 70 75 80	
acc cac ctt gca gag acg ctg ggg ctc tcc tca agc cca caa tct gga	288
Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser Ser Pro Gln Ser Gly	
85 90 95	
aat tct cag aac acc acg gac tct gaa gta gcg ttt cct cct ctt cca	336
Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala Phe Pro Pro Leu Pro	
100 105 110	
gcc agc gtg aat aac atg cct ggg ccg gct gag cca gaa gaa tct gta	384
Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu Pro Glu Glu Ser Val	
115 120 125	
gat gct ctc aag ctt tgt cct cgt gaa aac ttc gtg aaa ctg tgt aaa	432
Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe Val Lys Leu Cys Lys	
130 135 140	
cag agg gct gaa gag atc tac cca ata aag gag aga aag gat cgt act	480
Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu Arg Lys Asp Arg Thr	
145 150 155 160	
cgt ctg gct ctc atc ata tgc aat acg acg ttc gat cat ctt tct ctc	528
Arg Leu Ala Leu Ile Ile Cys Asn Thr Thr Phe Asp His Leu Ser Leu	
165 170 175	
agg aag ggg gct gac ctt gac gtt gca ggg atg agg agg ctg ctt aca	576
Arg Lys Gly Ala Asp Leu Asp Val Ala Gly Met Arg Arg Leu Leu Thr	
180 185 190	
gac ctt ggc tac agt gtg cac ata aaa gag gaa ctc act gct aag gac	624
Asp Leu Gly Tyr Ser Val His Ile Lys Glu Glu Leu Thr Ala Lys Asp	
195 200 205	
atg gaa tca gag ctg agg gca ttt gct gcc cgt cca gag cac aag tcc	672
Met Glu Ser Glu Leu Arg Ala Phe Ala Ala Arg Pro Glu His Lys Ser	
210 215 220	

tcg gac agc aca ttc ctg gtg ttc atg tct cat ggc atc ctg agt gga	720
Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Gly Ile Leu Ser Gly	
225 230 235 240	
atc tgt ggg acg aag tac agc gct gaa gga gac cca gat gta ttg gct	768
Ile Cys Gly Thr Lys Tyr Ser Ala Glu Gly Asp Pro Asp Val Leu Ala	
245 250 255	
tat gac acc atc ttc cag att ttc aac aac cgc aac tgc ctt agt cta	816
Tyr Asp Thr Ile Phe Gln Ile Phe Asn Asn Arg Asn Cys Leu Ser Leu	
260 265 270	
aag gac aag ccc aag gtc atc atc gtc cag gcc tgc aga ggt gaa aat	864
Lys Asp Lys Pro Lys Val Ile Ile Val Gln Ala Cys Arg Gly Glu Asn	
275 280 285	
ttg ggg gaa ctg ttg atc agt gac tct cca gcg gcc cca atg gac agc	912
Leu Gly Glu Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser	
290 295 300	
act tca cag atg ggt agc agc ctt tca cag gtg ggt gac aac cta gag	960
Thr Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu	
305 310 315 320	
gac gac gcc att tac aag gtc cac gtg gag aag gac ttc atc gct ttc	1008
Asp Asp Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe	
325 330 335	
tgc tcc tcg acc cca cat cat gtg tct tgg aga gac gtg aac aag gga	1056
Cys Ser Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly	
340 345 350	
tct ctc ttc att aca caa ctc atc acg tgc ttc caa aag tat tcg tgg	1104
Ser Leu Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp	
355 360 365	
tgc ttt cat ctg gag gaa gta ttt cgg aag gta caa cag tca ttt gaa	1152
Cys Phe His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu	
370 375 380	
aaa cca aat gtt aga gcc cag atg ccc acc att gaa cga cta tcc atg	1200
Lys Pro Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met	
385 390 395 400	
aca aga tac ttc tat ctc ttc cct ggc aat	1230
Thr Arg Tyr Phe Tyr Leu Phe Pro Gly Asn	
405 410	

<210> 24
 <211> 410
 <212> PRT
 <213> Felis catus

<400> 24

Met Ala Asp Lys Asp Leu Lys Gly Lys Arg Lys Gln Phe Ile Asn Ser

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	20							25					30				
Asn	Val	Leu	Asn	Gln	Glu	Glu	Met	Glu	Arg	Val	Lys	Cys	Glu	Asn	Ala		
	35						40					45					
Thr	Val	Met	Asp	Lys	Ala	Arg	Ala	Leu	Ile	Asp	Ser	Val	Leu	Arg	Lys		
	50					55					60						
Gly	Pro	Arg	Ala	Cys	Gln	Ile	Phe	Ile	Cys	His	Ile	Cys	Glu	Glu	Asp		
65					70					75					80		
Thr	His	Leu	Ala	Glu	Thr	Leu	Gly	Leu	Ser	Ser	Ser	Pro	Gln	Ser	Gly		
				85					90					95			
Asn	Ser	Gln	Asn	Thr	Thr	Asp	Ser	Glu	Val	Ala	Phe	Pro	Pro	Leu	Pro		
			100					105					110				
Ala	Ser	Val	Asn	Asn	Met	Pro	Gly	Pro	Ala	Glu	Pro	Glu	Glu	Ser	Val		
		115					120					125					
Asp	Ala	Leu	Lys	Leu	Cys	Pro	Arg	Glu	Asn	Phe	Val	Lys	Leu	Cys	Lys		
	130					135					140						
Gln	Arg	Ala	Glu	Glu	Ile	Tyr	Pro	Ile	Lys	Glu	Arg	Lys	Asp	Arg	Thr		
145					150					155					160		
Arg	Leu	Ala	Leu	Ile	Ile	Cys	Asn	Thr	Thr	Phe	Asp	His	Leu	Ser	Leu		
				165					170					175			
Arg	Lys	Gly	Ala	Asp	Leu	Asp	Val	Ala	Gly	Met	Arg	Arg	Leu	Leu	Thr		
			180					185					190				
Asp	Leu	Gly	Tyr	Ser	Val	His	Ile	Lys	Glu	Glu	Leu	Thr	Ala	Lys	Asp		
	195						200					205					
Met	Glu	Ser	Glu	Leu	Arg	Ala	Phe	Ala	Ala	Arg	Pro	Glu	His	Lys	Ser		
	210					215					220						
Ser	Asp	Ser	Thr	Phe	Leu	Val	Phe	Met	Ser	His	Gly	Ile	Leu	Ser	Gly		
225					230					235					240		

Ile Cys Gly Thr Lys Tyr Ser Ala Glu Gly Asp Pro Asp Val Leu Ala
245 250 255

Tyr Asp Thr Ile Phe Gln Ile Phe Asn Asn Arg Asn Cys Leu Ser Leu
260 265 270

Lys Asp Lys Pro Lys Val Ile Ile Val Gln Ala Cys Arg Gly Glu Asn
275 280 285

Leu Gly Glu Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser
290 295 300

Thr Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu
305 310 315 320

Asp Asp Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe
325 330 335

Cys Ser Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly
340 345 350

Ser Leu Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp
355 360 365

Cys Phe His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu
370 375 380

Lys Pro Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met
385 390 395 400

Thr Arg Tyr Phe Tyr Leu Phe Pro Gly Asn
405 410

<210> 25
<211> 1230
<212> DNA
<213> Felis catus

<400> 25
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ggctctaaca tttggttttt caaatgactg ttgtaccttc cgaaatactt cctccagatg 120
aaagcaccac gaatactttt ggaagcacgt gatgagttgt gtaatgaaga gagatccctt 180


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gttcacgtct ctccaagaca catgatgtgg ggtcgaggag cagaaagcga tgaagtcctt 240
ctccacgtgg accttgtaaa tggcgtcgtc ctctagggtt tcacccacct gtgaaaggct 300
gctacccatc tgtgaagtgc tgtccattgg ggccgctgga gagtcaactga tcaacagttc 360
ccccaaattt tcacctctgc aggccctggac gatgatgacc ttgggcttgt cctttagact 420
aaggcagttg cgggttggtga aaatctggaa gatggtgtca taagccaata catctgggtc 480
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cagcctcctc atccctgcaa cgtcaagggtc agcccccttc ctgagagaaa gatgatcgaa 720
cgtcgtattg catatgatga gagccagacg agtacgatcc tttctctcct ttattgggta 780
gatctcttca gccctctggt tacacagttt cacgaagttt tcacgaggac aaagcttgag 840
agcatctaca gattcttctg gctcagccgg ccagggcatg ttattcacgc tggctggaag 900
aggaggaaac gctacttcag agtccgtggt gttctgagaa tttccagatt gtgggcttga 960
ggagagcccc agcgtctctg caagggtgggt gtcttcctca cagatgtgac agataaagat 1020
ctggcacgcc cgtggccctt tccgcaggac gctgtcgatc agagctcggg ccttgtccat 1080
aacggtagcg ttttcacatt ttactctctc catctcctcc tgggttcagca cgtttttctc 1140
aaagagttca tccagcaagc cgttgaccgt ccccatgccg actgagttga tgaactgctt 1200
cctcttgccc ttcagatcct tgtcggccat 1230

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<210> 26
<211> 921
<212> DNA
<213> Felis catus

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<220>
<221> CDS
<222> (1)..(921)

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<400> 26
ata tgg gaa ctg gag aaa aac gtt tat gtt gta gag ttg gac tgg cac 48
Ile Trp Glu Leu Glu Lys Asn Val Tyr Val Val Glu Leu Asp Trp His
1 5 10 15

cct gat gcc ccc gga gaa atg gtg gtc ctc acc tgc aat act cct gaa 96
Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asn Thr Pro Glu
20 25 30

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gaa gat gac atc acc tgg acc tct gac cag agc agt gaa gtc cta ggc Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln Ser Ser Glu Val Leu Gly 35 40 45	144
tct ggt aaa act ctg acc atc caa gtc aaa gaa ttt gca gat gct ggc Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Ala Asp Ala Gly 50 55 60	192
cag tat acc tgt cat aaa gga ggc gag gtt ctg agc cat tcg ttc ctc Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Phe Leu 65 70 75 80	240
ctg ata cac aaa aag gaa gat gga att tgg tcc act gat atc tta agg Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Arg 85 90 95	288
gaa cag aaa gaa tcc aaa aat aag atc ttt cta aaa tgt gag gca aag Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys 100 105 110	336
aat tat tct gga cgt ttc acc tgc tgg tgg ctg acg gca atc agt acc Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr 115 120 125	384
gat ttg aaa ttc act gtc aaa agc agc aga ggc tcc tct gac ccc caa Asp Leu Lys Phe Thr Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln 130 135 140	432
gag gtg act tgt gga gca gcg aca ctc tca gca gag aag gtc aga gtg Glu Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Lys Val Arg Val 145 150 155 160	480
gac aac agg gat tat aag aag tac aca gtg gag tgt cag gag ggc agt Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser 165 170 175	528
gcc tgc ccg gct gcc gag gag agc cta ccc att gaa gtc gtg gtg gac Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp 180 185 190	576
gct att cac aag ctc aag tac gaa aac tac acc agc agc ttc ttc atc Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile 195 200 205	624
agg gac atc atc aaa ccg gac cca ccc aag aac ctg caa ctg aag cca Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro 210 215 220	672
tta aaa aat tct cgg cat gtg gaa gtg agc tgg gaa tac cct gac acc Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr 225 230 235 240	720
tgg agc acc cca cat tcc tac ttc tcc tta aca ttt ggc gta cag gtc Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Gly Val Gln Val 245 250 255	768
cag ggc aag aac aac aga gaa aag aaa gac aga ctc tcc gtg gac aag	816

Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Ser Val Asp Lys	
260 265 270	
acc tca gcc aag gtc gtg tgc cac aag gat gcc aag atc cgc gtg caa	864
Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln	
275 280 285	
gcc aga gac cgc tac tat agc tca tcc tgg agc aac tgg gca tcc gtg	912
Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asn Trp Ala Ser Val	
290 295 300	
tcc tgc agt	921
Ser Cys Ser	
305	

<210> 27
 <211> 307
 <212> PRT
 <213> Felis catus

<400> 27

Ile Trp Glu Leu Glu Lys Asn Val Tyr Val Val Glu Leu Asp Trp His
1 5 10 15

Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asn Thr Pro Glu
20 25 30

Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln Ser Ser Glu Val Leu Gly
35 40 45

Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Ala Asp Ala Gly
50 55 60

Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Phe Leu
65 70 75 80

Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Arg
85 90 95

Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys
100 105 110

Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr
115 120 125

Asp Leu Lys Phe Thr Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln
130 135 140

Glu Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Lys Val Arg Val
 145 150 155 160

Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser
 165 170 175

Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp
 180 185 190

Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile
 195 200 205

Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro
 210 215 220

Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr
 225 230 235 240

Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Gly Val Gln Val
 245 250 255

Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Ser Val Asp Lys
 260 265 270

Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln
 275 280 285

Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asn Trp Ala Ser Val
 290 295 300

Ser Cys Ser
 305

<210> 28
 <211> 921
 <212> DNA
 <213> Felis catus

<400> 28
 actgcaggac acggatgccc agttgctcca ggatgagcta tagtagcggg ctctggccttg 60
 cacgcggatc ttggcatcct tgtggcacac gaccttggct gaggtcttgt ccacggagag 120
 tctgtctttc ttttctctgt tggtcttgcc ctggacctgt acgccaaatg ttaaggagaa 180

gtaggaatgt ggggtgctcc aggtgtcagg gtattcccag ctacttcca catgccgaga	240
atTTTTtaat ggcttcagtt gcaggttctt ggggtgggtcc ggtttgatga tgtccctgat	300
gaagaagctg ctggtgtagt tttcgtactt gagcttgtga atagcgtcca ccacgacttc	360
aatgggtagg ctctcctcgg cagccgggca ggcactgccc tctgacact ccactgtgta	420
cttcttataa tccctgttgt ccactctgac cttctctgct gagagtgtcg ctgctccaca	480
agtcacctct tgggggtcag aggagcctct gctgcttttg acagtgaatt tcaaacgggt	540
actgattgcc gtcagccacc agcagggtgaa acgtccagaa taattctttg cctcacattt	600
tagaaagatc ttatttttgg attctttctg ttcctttaag atatcagtgg accaaattcc	660
atcttctttt ttgtgtatca ggaggaacga atggctcaga acctcgctc ctttatgaca	720
ggtatactgg ccagcatctg caaattcttt gacttggatg gtcagagttt taccagagcc	780
taggacttca ctgctctggt cagagggtcca ggtgatgtca tcttcttcag gagtattgca	840
ggtgaggacc accatttctc cgggggcac cagggtgccag tccaactcta caacataaac	900
gtttttctcc agttcccata t	921

<210> 29
 <211> 987
 <212> DNA
 <213> Felis catus

<220>
 <221> CDS
 <222> (1)..(987)

<400> 29 atg cat cct cag cag ttg gtc atc gcc tgg ttt tcc ctg gtt ttg ctg Met His Pro Gln Gln Leu Val Ile Ala Trp Phe Ser Leu Val Leu Leu 1 5 10 15	48
gca cct ccc ctc atg gcc ata tgg gaa ctg gag aaa aac gtt tat gtt Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val 20 25 30	96
gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctc Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu 35 40 45	144
acc tgc aat act cct gaa gaa gat gac atc acc tgg acc tct gac cag Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln 50 55 60	192
agc agt gaa gtc cta ggc tct ggt aaa act ctg acc atc caa gtc aaa Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys	240

65	70	75	80	
gaa ttt gca gat gct ggc cag tat acc tgt cat aaa gga ggc gag gtt				288
Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val	85	90	95	
ctg agc cat tcg ttc ctc ctg ata cac aaa aag gaa gat gga att tgg				336
Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp	100	105	110	
tcc act gat atc tta agg gaa cag aaa gaa tcc aaa aat aag atc ttt				384
Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe	115	120	125	
cta aaa tgt gag gca aag aat tat tct gga cgt ttc acc tgc tgg tgg				432
Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp	130	135	140	
ctg acg gca atc agt acc gat ttg aaa ttc act gtc aaa agc agc aga				480
Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg	145	150	155	160
ggc tcc tct gac ccc caa ggg gtg act tgt gga gca gcg aca ctc tca				528
Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser	165	170	175	
gca gag aag gtc aga gtg gac aac agg gat tat aag aag tac aca gtg				576
Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val	180	185	190	
gag tgt cag gag ggc agt gcc tgc ccg gct gcc gag gag agc cta ccc				624
Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro	195	200	205	
att gaa gtc gtg gtg gac gct att cac aag ctc aag tac gaa aac tac				672
Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr	210	215	220	
acc agc agc ttc ttc atc agg gac atc atc aaa ccg gac cca ccc aag				720
Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys	225	230	235	240
aac ctg caa ctg aag cca tta aaa aat tct cgg cat gtg gaa gtg agc				768
Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser	245	250	255	
tgg gaa tac cct gac acc tgg agc acc cca cat tcc tac ttc tcc tta				816
Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu	260	265	270	
aca ttt ggc gta cag gtc cag ggc aag aac aac aga gaa aag aaa gac				864
Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp	275	280	285	
aga ctc tcc gtg gac aag acc tca gcc aag gtc gtg tgc cac aag gat				912
Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp	290	295	300	

gcc aag atc cgc gtg caa gcc aga gac cgc tac tat agc tca tcc tgg 960
 Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
 305 310 315 320

agc aac tgg gca tcc gtg tcc tgc agt 987
 Ser Asn Trp Ala Ser Val Ser Cys Ser
 325

<210> 30
 <211> 329
 <212> PRT
 <213> Felis catus

<400> 30

Met His Pro Gln Gln Leu Val Ile Ala Trp Phe Ser Leu Val Leu Leu
 1 5 10 15

Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val
 20 25 30

Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
 35 40 45

Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln
 50 55 60

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
 65 70 75 80

Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
 85 90 95

Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
 100 105 110

Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
 115 120 125

Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
 130 135 140

Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg
 145 150 155 160

Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser
165 170 175

Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
180 185 190

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro
195 200 205

Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys
225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
260 265 270

Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
275 280 285

Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp
290 295 300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
305 310 315 320

Ser Asn Trp Ala Ser Val Ser Cys Ser
325

<210> 31
<211> 987
<212> DNA
<213> Felis catus

<400> 31
actgcaggac acggatgccc agttgctcca ggatgagcta tagtagcggt ctctggcttg 60
cacgcggatc ttggcatcct tgtggcacac gaccttggt gaggtcttgt ccacggagag 120
tctgtctttc ttttctctgt tgttcttgcc ctggacctgt acgccaaatg ttaaggagaa 180
gtaggaatgt ggggtgctcc aggtgtcagg gtattcccag ctacttcca catgccgaga 240

attttttaaat ggcttcagtt gcaggttctt ggggtgggtcc ggtttgatga tgtccctgat 300
 gaagaagctg ctggtgtagt tttcgtactt gagcttgtga atagcgtcca ccacgacttc 360
 aatgggtagg ctctcctcgg cagccgggca ggcactgccc tcctgacact ccactgtgta 420
 cttcttataa tccctgttgt ccactctgac cttctctgct gagagtgtcg ctgctccaca 480
 agtcacccct tggggggtcag aggagcctct gctgcttttg acagtgaatt tcaaatcggt 540
 actgattgcc gtcagccacc agcaggtgaa acgtccagaa taattctttg cctcacattt 600
 tagaaagatc ttatttttgg attctttctg ttcctttaag atatcagtgg accaaattcc 660
 atcttctttt ttgtgtatca ggaggaacga atggctcaga acctcgctc ctttatgaca 720
 ggtatactgg ccagcatctg caaattcttt gacttggatg gtcagagttt taccagagcc 780
 taggacttca ctgctctggt cagaggtcca ggtgatgtca tcttcttcag gagtattgca 840
 ggtgaggacc accatttctc cgggggcac cagggtgccag tccaactcta caacataaac 900
 gtttttctcc agttcccata tggccatgag gggaggtgcc agcaaaacca gggaaaacca 960
 ggcgatgacc aactgctgag gatgcat 987

<210> 32
 <211> 666
 <212> DNA
 <213> Felis catus

<220>
 <221> CDS
 <222> (1)..(666)

<400> 32
 atg tgc ccg ccg cgt ggc ctc ctc ctt gta acc atc ctg gtc ctg tta 48
 Met Cys Pro Pro Arg Gly Leu Leu Leu Val Thr Ile Leu Val Leu Leu
 1 5 10 15
 aac cac ctg gac cac ctc agt ttg gcc agg aac ctc ccc aca ccc aca 96
 Asn His Leu Asp His Leu Ser Leu Ala Arg Asn Leu Pro Thr Pro Thr
 20 25 30
 cca agc cca gga atg ttc cag tgc ctc aac cac tcc caa acc ctg ctg 144
 Pro Ser Pro Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu Leu
 35 40 45
 cga gcc atc agc aac acg ctt cag aag gcc aga caa act cta gaa ttt 192
 Arg Ala Ile Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe
 50 55 60
 tac tcc tgc act tcc gaa gag att gat cat gaa gat atc aca aaa gat 240
 Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp

65	70	75	80	
aaa acc agc aca gtg gag gcc tgc tta cca ctg gaa tta acc atg aat				288
Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn				
	85	90	95	
gag agt tgc ctg gct tcc aga gag atc tct ctg ata act aat ggg agt				336
Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser				
	100	105	110	
tgc ctg gcc tcc aga aag acc tct ttt atg acg acc ctg tgc ctt agc				384
Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu Ser				
	115	120	125	
agt atc tat gag gac ttg aag atg tac cag gtg gag ttc aag gcc atg				432
Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala Met				
	130	135	140	
aat gca aag ctg tta atg gat cct aaa agg cag atc ttt ctg gat caa				480
Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln				
	145	150	155	160
aac atg ctg aca gct att gat gag ctg tta cag gcc ctg aat gtc aac				528
Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val Asn				
	165	170	175	
agt gtg act gtg cca cag aac tcc tcc ctg gaa gaa ccg gat ttt tat				576
Ser Val Thr Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe Tyr				
	180	185	190	
aaa act aaa atc aag ctc tgc ata ctt ctt cat gct ttc aga att cgt				624
Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg				
	195	200	205	
gca gtg acc atc aat aga atg atg agc tat ctg aat gct tcc				666
Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser				
	210	215	220	

<210> 33
 <211> 222
 <212> PRT
 <213> Felis catus

<400> 33

Met Cys Pro Pro Arg Gly Leu Leu Leu Val Thr Ile Leu Val Leu Leu
1 5 10 15

Asn His Leu Asp His Leu Ser Leu Ala Arg Asn Leu Pro Thr Pro Thr
20 25 30

Pro Ser Pro Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu Leu
35 40 45

Arg Ala Ile Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe
 50 55 60

Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp
 65 70 75 80

Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn
 85 90 95

Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser
 100 105 110

Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu Ser
 115 120 125

Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala Met
 130 135 140

Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln
 145 150 155 160

Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val Asn
 165 170 175

Ser Val Thr Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe Tyr
 180 185 190

Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg
 195 200 205

Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser
 210 215 220

<210> 34
 <211> 666
 <212> DNA
 <213> Felis catus

<400> 34
 ggaagcattc agatagctca tcattctatt gatggtcact gcacgaattc tgaaagcatg 60
 aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggttcttcca gggaggagtt 120
 ctgtggcaca gtcacactgt tgacattcag ggctgtaac agctcatcaa tagctgtcag 180

catgttttga tccagaaaga tctgcctttt aggatccatt aacagctttg cattcatggc	240
cttgaactcc acctggtaca tcttcaagtc ctcatagata ctgctaaggc acagggtcgt	300
cataaaagag gtctttctgg aggccaggca actcccatta gttatcagag agatctctct	360
ggaagccagg caactctcat tcatggttaa ttccagtggg aagcaggcct ccactgtgct	420
ggtttttatct tttgtgatat cttcatgata aatctcttcg gaagtgcagg agtaaaattc	480
tagagtttgt ctggccttct gaagcgtggt gctgatggct cgcagcaggg tttgggagtg	540
gttgaggcac tggaacattc ctgggcttgg tgtgggtgtg gggagggtcc tggccaaact	600
gaggtgggtcc aggtgggtta acaggaccag gatgggtaca aggaggaggc cacgcggcgg	660
gcacat	666

<210> 35
 <211> 591
 <212> DNA
 <213> Felis catus

<220>
 <221> CDS
 <222> (1)..(591)

<400> 35	
agg aac ctc ccc aca ccc aca cca agc cca gga atg ttc cag tgc ctc	48
Arg Asn Leu Pro Thr Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu	
1 5 10 15	
aac cac tcc caa acc ctg ctg cga gcc atc agc aac acg ctt cag aag	96
Asn His Ser Gln Thr Leu Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys	
20 25 30	
gcc aga caa act cta gaa ttt tac tcc tgc act tcc gaa gag att gat	144
Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp	
35 40 45	
cat gaa gat atc aca aaa gat aaa acc agc aca gtg gag gcc tgc tta	192
His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu	
50 55 60	
cca ctg gaa tta acc atg aat gag agt tgc ctg gct tcc aga gag atc	240
Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile	
65 70 75 80	
tct ctg ata act aat ggg agt tgc ctg gcc tcc aga aag acc tct ttt	288
Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe	
85 90 95	
atg acg acc ctg tgc ctt agc agt atc tat gag gac ttg aag atg tac	336
Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr	
100 105 110	

cag gtg gag ttc aag gcc atg aat gca aag ctg tta atg gat cct aaa	384
Gln Val Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys	
115 120 125	
agg cag atc ttt ctg gat caa aac atg ctg aca gct att gat gag ctg	432
Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu	
130 135 140	
tta cag gcc ctg aat gtc aac agt gtg act gtg cca cag aac tcc tcc	480
Leu Gln Ala Leu Asn Val Asn Ser Val Thr Val Pro Gln Asn Ser Ser	
145 150 155 160	
ttg gaa gaa ccg gat ttt tat aaa act aaa atc aag ctc tgc ata ctt	528
Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu	
165 170 175	
ctt cat gct ttc aga att cgt gca gtg acc atc aat aga atg atg agc	576
Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser	
180 185 190	
tat ctg aat gct tcc	591
Tyr Leu Asn Ala Ser	
195	

<210> 36
 <211> 197
 <212> PRT
 <213> Felis catus

<400> 36

Arg Asn Leu Pro Thr Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu	
1 5 10 15	
Asn His Ser Gln Thr Leu Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys	
20 25 30	
Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp	
35 40 45	
His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu	
50 55 60	
Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile	
65 70 75 80	
Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe	
85 90 95	

Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr
 100 105 110

Gln Val Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys
 115 120 125

Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu
 130 135 140

Leu Gln Ala Leu Asn Val Asn Ser Val Thr Val Pro Gln Asn Ser Ser
 145 150 155 160

Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu
 165 170 175

Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser
 180 185 190

Tyr Leu Asn Ala Ser
 195

<210> 37
 <211> 591
 <212> DNA
 <213> Felis catus

<400> 37
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 aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggttcttcca aggaggagtt 120
 ctgtggcaca gtcacactgt tgacattcag ggctgtaac agctcatcaa tagctgtcag 180
 catgttttga tccagaaaga tctgcctttt aggatccatt aacagctttg cattcatggc 240
 cttgaactcc acctggtaca tcttcaagtc ctcatagata ctgctaaggc acagggtcgt 300
 cataaaagag gtcttttctgg aggccaggca actccatta gttatcagag agatctctct 360
 ggaagccagg caactctcat tcatggttaa ttccagtggg aagcaggcct ccaactgtgct 420
 gggttttatct tttgtgatat cttcatgata aatctcttcg gaagtgcagg agtaaaattc 480
 tagagtttgt ctggccttct gaagcgtggt gctgatggct cgcagcaggg tttgggagtg 540
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<210> 38
 <211> 1599

<212> DNA
 <213> Felis catus

<220>
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Met His Pro Gln Gln Leu Val Ile Ala Trp Leu Ser Leu Val Leu Leu
1          5          10          15

gca cct ccc ctc atg gcc ata tgg gaa ctg gag aaa aac gtt tat gtt      96
Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val
          20          25          30

gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctc      144
Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
          35          40          45

acc tgc aat act cct gaa gaa gat gac atc acc tgg acc tct gac cag      192
Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln
          50          55          60

agc agt gaa gtc cta ggc tct ggt aaa act ctg acc atc caa gtc aaa      240
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65          70          75          80

gaa ttt gca gat gct ggc cag tat acc tgt cat aaa gga ggc gag gtt      288
Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
          85          90          95

ctg agc cat tcg ttc ctc ctg ata cac aaa aag gaa gat gga att tgg      336
Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
          100          105          110

tcc act gat atc tta agg gaa cag aaa gaa tcc aaa aat aag atc ttt      384
Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
          115          120          125

cta aaa tgt gag gca aag aat tat tct gga cgt ttc acc tgc tgg tgg      432
Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
          130          135          140

ctg acg gca atc agt acc gat ttg aaa ttc act gtc aaa agc agc aga      480
Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg
145          150          155          160

ggc tcc tct gac ccc caa gag gtg act tgt gga gca gcg aca ctc tca      528
Gly Ser Ser Asp Pro Gln Glu Val Thr Cys Gly Ala Ala Thr Leu Ser
          165          170          175

gca gag aag gtc aga gtg gac aac agg gat tat aag aag tac aca gtg      576
Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
          180          185          190

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gag tgt cag gag ggc agt gcc tgc ccg gct gcc gag gag agc cta ccc Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro 195 200 205	624
att gaa gtc gtg gtg gac gct att cac aag ctc aag tac gaa aac tac Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr 210 215 220	672
acc agc agc ttc ttc atc agg gac atc atc aaa ccg gac cca ccc aag Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys 225 230 235 240	720
aac ctg caa ctg aag cca tta aaa aat tct cgg cat gtg gaa gtg agc Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser 245 250 255	768
tgg gaa tac cct gac acc tgg agc acc cca cat tcc tac ttc tcc tta Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu 260 265 270	816
aca ttt ggc gta cag gtc cag ggc aag aac aac aga gaa aag aaa gac Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp 275 280 285	864
aga ctc tcc gtg gac aag acc tca gcc aag gtc gtg tgc cac aag gat Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp 290 295 300	912
gcc aag atc cgc gtg caa gcc aga gac cgc tac tat agc tca tcc tgg Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp 305 310 315 320	960
agc aac tgg gca tcc gtg tcc tgc agt ggt ggc ggt ggc ggc gga tct Ser Asn Trp Ala Ser Val Ser Cys Ser Gly Gly Gly Gly Gly Gly Ser 325 330 335	1008
aga aac ttg cca acc cct act cca tcc ccg ggg atg ttc cag tgc ctc Arg Asn Leu Pro Thr Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu 340 345 350	1056
aac cac tcc caa acc ctg ctg cga gcc atc agc aac acg ctt cag aag Asn His Ser Gln Thr Leu Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys 355 360 365	1104
gcc aga caa act cta gaa ttt tac tcc tgc act tcc gaa gag att gat Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp 370 375 380	1152
cat gaa gat atc aca aaa gat aaa acc agc aca gtg gag gcc tgc tta His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu 385 390 395 400	1200
cca ctg gaa tta acc atg aat gag agt tgc ctg gct tcc aga gag atc Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile 405 410 415	1248
tct ctg ata act aat ggg agt tgc ctg gcc tcc aga aag acc tct ttt	1296

Ser	Leu	Ile	Thr	Asn	Gly	Ser	Cys	Leu	Ala	Ser	Arg	Lys	Thr	Ser	Phe	
			420					425					430			
atg	acg	acc	ctg	tgc	ctt	agc	agt	atc	tat	gag	gac	ttg	aag	atg	tac	1344
Met	Thr	Thr	Leu	Cys	Leu	Ser	Ser	Ile	Tyr	Glu	Asp	Leu	Lys	Met	Tyr	
		435					440					445				
cag	gtg	gag	ttc	aag	gcc	atg	aat	gca	aag	ctg	tta	atg	gat	cct	aaa	1392
Gln	Val	Glu	Phe	Lys	Ala	Met	Asn	Ala	Lys	Leu	Leu	Met	Asp	Pro	Lys	
	450					455					460					
agg	cag	atc	ttt	ctg	gat	caa	aac	atg	ctg	aca	gct	att	gat	gag	ctg	1440
Arg	Gln	Ile	Phe	Leu	Asp	Gln	Asn	Met	Leu	Thr	Ala	Ile	Asp	Glu	Leu	
465				470					475					480		
tta	cag	gcc	ctg	aat	gtc	aac	agt	gtg	act	gtg	cca	cag	aac	tcc	tcc	1488
Leu	Gln	Ala	Leu	Asn	Val	Asn	Ser	Val	Thr	Val	Pro	Gln	Asn	Ser	Ser	
			485					490					495			
ttg	gaa	gaa	ccg	gat	ttt	tat	aaa	act	aaa	atc	aag	ctc	tgc	ata	ctt	1536
Leu	Glu	Glu	Pro	Asp	Phe	Tyr	Lys	Thr	Lys	Ile	Lys	Leu	Cys	Ile	Leu	
		500						505				510				
ctt	cat	gct	ttc	aga	att	cgt	gca	gtg	acc	atc	aat	aga	atg	atg	agc	1584
Leu	His	Ala	Phe	Arg	Ile	Arg	Ala	Val	Thr	Ile	Asn	Arg	Met	Met	Ser	
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tat	ctg	aat	gct	tcc												1599
Tyr	Leu	Asn	Ala	Ser												
	530															

<210> 39
 <211> 533
 <212> PRT
 <213> Felis catus

<400> 39

Met	His	Pro	Gln	Gln	Leu	Val	Ile	Ala	Trp	Leu	Ser	Leu	Val	Leu	Leu	
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			20					25					30			
Val	Glu	Leu	Asp	Trp	His	Pro	Asp	Ala	Pro	Gly	Glu	Met	Val	Val	Leu	
	35						40					45				
Thr	Cys	Asn	Thr	Pro	Glu	Glu	Asp	Asp	Ile	Thr	Trp	Thr	Ser	Asp	Gln	
	50					55					60					
Ser	Ser	Glu	Val	Leu	Gly	Ser	Gly	Lys	Thr	Leu	Thr	Ile	Gln	Val	Lys	
65					70					75					80	

Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
 85 90 95
 Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
 100 105 110
 Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
 115 120 125
 Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
 130 135 140
 Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg
 145 150 155 160
 Gly Ser Ser Asp Pro Gln Glu Val Thr Cys Gly Ala Ala Thr Leu Ser
 165 170 175
 Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
 180 185 190
 Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro
 195 200 205
 Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
 210 215 220
 Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys
 225 230 235 240
 Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
 245 250 255
 Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
 260 265 270
 Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
 275 280 285
 Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp
 290 295 300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
 305 310 315 320

Ser Asn Trp Ala Ser Val Ser Cys Ser Gly Gly Gly Gly Gly Ser
 325 330 335

Arg Asn Leu Pro Thr Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu
 340 345 350

Asn His Ser Gln Thr Leu Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys
 355 360 365

Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp
 370 375 380

His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu
 385 390 395 400

Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile
 405 410 415

Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe
 420 425 430

Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr
 435 440 445

Gln Val Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys
 450 455 460

Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu
 465 470 475 480

Leu Gln Ala Leu Asn Val Asn Ser Val Thr Val Pro Gln Asn Ser Ser
 485 490 495

Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu
 500 505 510

Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser
 515 520 525

Tyr Leu Asn Ala Ser
530

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<211> 1599
<212> DNA
<213> Felis catus

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ctgtggcaca gtcacactgt tgacattcag ggctgtaac agctcatcaa tagctgtcag 180
catgttttga tccagaaaga tctgcctttt aggatccatt aacagctttg cattcatggc 240
cttgaactcc acctggtaca tcttcaagtc ctcatagata ctgctaaggc acagggctcg 300
cataaaagag gtctttcttg aggccaggca actccatta gttatcagag agatctctct 360
ggaagccagg caactctcat tcatggttaa ttccagtggc aagcaggcct ccactgtgct 420
ggttttatct tttgtgatat ctcatgac aatctcttcg gaagtgcagg agtaaaattc 480
tagagtttgt ctggccttct gaagcgtggt gctgatggct cgcagcaggg tttgggagtg 540
gttgaggcac tggaacatcc ccggggatgg agtaggggtt ggcaagtttc tagatccgcc 600
gccaccgcca ccactgcagg acacggatgc ccagttgctc caggatgagc tatagtagcg 660
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gtccacggag agtctgtctt tcttttctct gttgttcttg ccctggacct gtacgcaaaa 780
tgttaaggag aagtaggaat gtgggggtgct ccaggtgtca gggattccc agctcatttc 840
cacatgccga gaatttttta atggcttcag ttgcaggctt ttgggtgggt ccggtttgat 900
gatgtccctg atgaagaagc tgctggtgta gttttcgtac ttgagcttgt gaatagcgtc 960
caccacgact tcaatgggta ggctctctc gccagccggg caggcactgc cctcctgaca 1020
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cgctgctcca caagtcacct cttgggggtc agaggagcct ctgctgcttt tgacagtga 1140
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tgctcacat tttagaaaga tcttattttt ggattcttct tgttccctta agatatcagt 1260
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tttaccagag cctaggactt cactgctctg gtcagaggtc caggatgatgt catcttcttc 1440

aggagtattg caggtgagga ccaccatttc tccgggggca tcagggtgcc agtccaactc 1500
 tacaacataa acgtttttct ccagttccca tatggccatg aggggaggtg ccagcaaaac 1560
 cagggaaagc caggcgatga ccaactgctg aggatgcat 1599

<210> 41
 <211> 576
 <212> DNA
 <213> Felis catus

<400> 41
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 aagactcaaa ttgtatctta tcatcatgtc ctggaacact tctctgaaag aatatgatgt 180
 catttccttc atcattgata ctctcaggag gactcatttc cttaaaggaa ataattttgt 240
 tctcacagga gagagtagac atgggtcttat aattcacaga gatggttact gccagacctc 300
 tagtgaggct atctttatac atatatatga taaattcagt ccgggggtgca ttatctgtac 360
 agtcagaatc aggcataatc tcaaacacag gttgatctcc ctgggtaatg aagagaactt 420
 ggtcgttcaa gtttcgtaag attgagagtt tatgttcaag cttgccaaag taatctgttt 480
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 caaagttgat gcaatcatct actggtatag cagtca 576

<210> 42
 <211> 0
 <212> DNA
 <213> Felis catus

<400> 42
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<210> 43
 <211> 1533
 <212> DNA
 <213> Felis catus

<220>
 <221> CDS
 <222> (1)..(1533)

<400> 43
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 Ile Trp Glu Leu Glu Lys Asn Val Tyr Val Val Glu Leu Asp Trp His
 1 5 10 15

cct gat gcc ccc gga gaa atg gtg gtc ctc acc tgc aat act cct gaa Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asn Thr Pro Glu 20 25 30	96
gaa gat gac atc acc tgg acc tct gac cag agc agt gaa gtc cta ggc Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln Ser Ser Glu Val Leu Gly 35 40 45	144
tct ggt aaa act ctg acc atc caa gtc aaa gaa ttt gca gat gct ggc Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Ala Asp Ala Gly 50 55 60	192
cag tat acc tgt cat aaa gga ggc gag gtt ctg agc cat tcg ttc ctc Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Phe Leu 65 70 75 80	240
ctg ata cac aaa aag gaa gat gga att tgg tcc act gat atc tta agg Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Arg 85 90 95	288
gaa cag aaa gaa tcc aaa aat aag atc ttt cta aaa tgt gag gca aag Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys 100 105 110	336
aat tat tct gga cgt ttc acc tgc tgg tgg ctg acg gca atc agt acc Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr 115 120 125	384
gat ttg aaa ttc act gtc aaa agc agc aga ggc tcc tct gac ccc caa Asp Leu Lys Phe Thr Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln 130 135 140	432
gag gtg act tgt gga gca gcg aca ctc tca gca gag aag gtc aga gtg Glu Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Lys Val Arg Val 145 150 155 160	480
gac aac agg gat tat aag aag tac aca gtg gag tgt cag gag ggc agt Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser 165 170 175	528
gcc tgc ccg gct gcc gag gag agc cta ccc att gaa gtc gtg gtg gac Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp 180 185 190	576
gct att cac aag ctc aag tac gaa aac tac acc agc agc ttc ttc atc Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile 195 200 205	624
agg gac atc atc aaa ccg gac cca ccc aag aac ctg caa ctg aag cca Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro 210 215 220	672
tta aaa aat tct cgg cat gtg gaa gtg agc tgg gaa tac cct gac acc Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr 225 230 235 240	720

tgg agc acc cca cat tcc tac ttc tcc tta aca ttt ggc gta cag gtc	768
Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Gly Val Gln Val	
245 250 255	
cag ggc aag aac aac aga gaa aag aaa gac aga ctc tcc gtg gac aag	816
Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Ser Val Asp Lys	
260 265 270	
acc tca gcc aag gtc gtg tgc cac aag gat gcc aag atc cgc gtg caa	864
Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln	
275 280 285	
gcc aga gac cgc tac tat agc tca tcc tgg agc aac tgg gca tcc gtg	912
Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asn Trp Ala Ser Val	
290 295 300	
tcc tgc agt ggt ggc ggt ggc ggc gga tct aga aac ttg cca acc cct	960
Ser Cys Ser Gly Gly Gly Gly Gly Gly Ser Arg Asn Leu Pro Thr Pro	
305 310 315 320	
act cca tcc ccg ggg atg ttc cag tgc ctc aac cac tcc caa acc ctg	1008
Thr Pro Ser Pro Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu	
325 330 335	
ctg cga gcc atc agc aac acg ctt cag aag gcc aga caa act cta gaa	1056
Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu	
340 345 350	
ttt tac tcc tgc act tcc gaa gag att gat cat gaa gat atc aca aaa	1104
Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys	
355 360 365	
gat aaa acc agc aca gtg gag gcc tgc tta cca ctg gaa tta acc atg	1152
Asp Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met	
370 375 380	
aat gag agt tgc ctg gct tcc aga gag atc tct ctg ata act aat ggg	1200
Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly	
385 390 395 400	
agt tgc ctg gcc tcc aga aag acc tct ttt atg acg acc ctg tgc ctt	1248
Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu	
405 410 415	
agc agt atc tat gag gac ttg aag atg tac cag gtg gag ttc aag gcc	1296
Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala	
420 425 430	
atg aat gca aag ctg tta atg gat cct aaa agg cag atc ttt ctg gat	1344
Met Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp	
435 440 445	
caa aac atg ctg aca gct att gat gag ctg tta cag gcc ctg aat gtc	1392
Gln Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val	
450 455 460	
aac agt gtg act gtg cca cag aac tcc tcc ttg gaa gaa ccg gat ttt	1440

Asn	Ser	Val	Thr	Val	Pro	Gln	Asn	Ser	Ser	Leu	Glu	Glu	Pro	Asp	Phe		
465					470					475					480		
tat	aaa	act	aaa	atc	aag	ctc	tgc	ata	ctt	ctt	cat	gct	ttc	aga	att		1488
Tyr	Lys	Thr	Lys	Ile	Lys	Leu	Cys	Ile	Leu	Leu	His	Ala	Phe	Arg	Ile		
				485					490					495			
cgt	gca	gtg	acc	atc	aat	aga	atg	atg	agc	tat	ctg	aat	gct	tcc			1533
Arg	Ala	Val	Thr	Ile	Asn	Arg	Met	Met	Ser	Tyr	Leu	Asn	Ala	Ser			
			500					505					510				

<210> 44
 <211> 511
 <212> PRT
 <213> Felis catus

<400> 44

Ile	Trp	Glu	Leu	Glu	Lys	Asn	Val	Tyr	Val	Val	Glu	Leu	Asp	Trp	His		
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			20					25					30				
Glu	Asp	Asp	Ile	Thr	Trp	Thr	Ser	Asp	Gln	Ser	Ser	Glu	Val	Leu	Gly		
	35						40					45					
Ser	Gly	Lys	Thr	Leu	Thr	Ile	Gln	Val	Lys	Glu	Phe	Ala	Asp	Ala	Gly		
	50					55					60						
Gln	Tyr	Thr	Cys	His	Lys	Gly	Gly	Glu	Val	Leu	Ser	His	Ser	Phe	Leu		
65					70					75					80		
Leu	Ile	His	Lys	Lys	Glu	Asp	Gly	Ile	Trp	Ser	Thr	Asp	Ile	Leu	Arg		
				85					90					95			
Glu	Gln	Lys	Glu	Ser	Lys	Asn	Lys	Ile	Phe	Leu	Lys	Cys	Glu	Ala	Lys		
			100					105					110				
Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Trp	Trp	Leu	Thr	Ala	Ile	Ser	Thr		
		115					120						125				
Asp	Leu	Lys	Phe	Thr	Val	Lys	Ser	Ser	Arg	Gly	Ser	Ser	Asp	Pro	Gln		
	130					135					140						
Glu	Val	Thr	Cys	Gly	Ala	Ala	Thr	Leu	Ser	Ala	Glu	Lys	Val	Arg	Val		
145					150					155					160		

Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser
 165 170 175

Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp
 180 185 190

Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile
 195 200 205

Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro
 210 215 220

Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr
 225 230 235 240

Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Gly Val Gln Val
 245 250 255

Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Ser Val Asp Lys
 260 265 270

Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln
 275 280 285

Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asn Trp Ala Ser Val
 290 295 300

Ser Cys Ser Gly Gly Gly Gly Gly Gly Ser Arg Asn Leu Pro Thr Pro
 305 310 315 320

Thr Pro Ser Pro Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu
 325 330 335

Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu
 340 345 350

Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys
 355 360 365

Asp Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met
 370 375 380

Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly
 385 390 395 400

Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu
 405 410 415

Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala
 420 425 430

Met Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp
 435 440 445

Gln Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val
 450 455 460

Asn Ser Val Thr Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe
 465 470 475 480

Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile
 485 490 495

Arg Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser
 500 505 510

<210> 45
 <211> 1533
 <212> DNA
 <213> Felis catus

<400> 45
 ggaagcattc agatagctca tcattctatt gatggtcact gcacgaattc tgaaagcatg 60
 aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggttcttcca aggaggagtt 120
 ctgtggcaca gtcacactgt tgacattcag ggccgtgaac agctcatcaa tagctgtcag 180
 catgttttga tccagaaaga tctgcctttt aggatccatt aacagctttg cattcatggc 240
 cttgaactcc acctggtaca tcttcaagtc ctcatagata ctgctaaggc acagggctcgt 300
 cataaaagag gtctttcttg aggccaggca actccatta gttatcagag agatctctct 360
 ggaagccagg caactctcat tcatggttaa ttccagtggc aagcaggcct cactgtgct 420
 ggttttatct tttgtgatat cttcatgac aatctcttcg gaagtgcagg agtaaaattc 480
 tagagtttgt ctggccttct gaagcgtggt gctgatggct cgcagcaggg tttgggagtg 540

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gttgaggcac tggaacatcc ccgggggatgg agtaggggtt ggcaagtttc tagatccgcc      600
gccaccgcca ccactgcagg acacgggatgc ccagttgctc caggatgagc tatagtagcg      660
gtctctggct tgcacgcgga tcttggcate cttgtggcac acgaccttgg ctgaggtctt      720
gtccacggag agtctgtctt tcttttctct gttgttcttg ccttggacct gtacgccaaa      780
tgttaaggag aagtaggaat gtgggggtgct ccaggtgtca gggatttccc agctcacttc      840
cacatgccga gaatttttta atggcttcag ttgcagggtc ttgggtgggt ccggtttgat      900
gatgtccctg atgaagaagc tgetgggtgta gttttcgta ttgagcttgt gaatagcgtc      960
caccacgact tcaatgggta ggctctctc gccagccggg caggcactgc cctcctgaca     1020
ctccactgtg tacttcttat aatccctgtt gtccactctg accttctctg ctgagagtgt     1080
cgctgctcca caagtcacct cttgggggtc agaggagcct ctgctgcttt tgacagtga      1140
tttcaaatcg gtactgattg ccgtcagcca ccagcaggtg aaacgtccag aataattctt     1200
tgcctcacat tttagaaaga tcttattttt ggattctttc tgttccctta agatatcagt     1260
ggaccaaatt ccatcttcct ttttgtgtat caggaggaac gaatggctca gaacctcgcc     1320
tcctttatga caggtatact ggccagcatc tgcaaattct ttgacttgga tggtcagagt     1380
tttaccagag cctaggactt cactgctctg gtcagaggtc caggatgatgt catcttcttc     1440
aggagtattg caggtgagga ccaccatttc tccgggggca tcagggtgcc agtccaactc     1500
tacaacataa acgtttttct ccagttccca tat                                  1533

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<210> 46
<211> 666
<212> DNA
<213> Canis familiaris

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<220>
<221> CDS
<222> (1)..(666)

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<400> 46
atg tgc ccg ccg cgc ggc ctc ctc ctt gtg acc atc ctg gtc ctg cta      48
Met Cys Pro Pro Arg Gly Leu Leu Leu Val Thr Ile Leu Val Leu Leu
1          5          10          15

agc cac ctg gac cac ctt act tgg gcc agg agc ctc ccc aca gcc tca      96
Ser His Leu Asp His Leu Thr Trp Ala Arg Ser Leu Pro Thr Ala Ser
          20          25          30

ccg agc cca gga ata ttc cag tgc ctc aac cac tcc caa aac ctg ctg     144
Pro Ser Pro Gly Ile Phe Gln Cys Leu Asn His Ser Gln Asn Leu Leu
          35          40          45

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aga gcc gtc agc aac acg ctt cag aag gcc aga caa act cta gaa tta	192
Arg Ala Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Leu	
50 55 60	
tat tcc tgc act tcc gaa gag att gat cat gaa gat atc aca aag gat	240
Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp	
65 70 75 80	
aaa acc agc aca gtg gag gcc tgc tta cca ctg gaa tta acc atg aat	288
Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn	
85 90 95	
gag agt tgc ctg gct tcc aga gag atc tct ttg ata act aac ggg agt	336
Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser	
100 105 110	
tgc ctg gcc tct gga aag gcc tct ttt atg acg gtc ctg tgc ctt agc	384
Cys Leu Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu Ser	
115 120 125	
agc atc tat gag gac ttg aag atg tac cag atg gaa ttc aag gcc atg	432
Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala Met	
130 135 140	
aac gca aag ctt tta atg gat ccc aag agg cag atc ttt ctg gat caa	480
Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln	
145 150 155 160	
aac atg ctg aca gct atc gat gag ctg tta cag gcc ctg aat ttc aac	528
Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe Asn	
165 170 175	
agt gtg act gtg cca cag aaa tcc tcc ctt gaa gag ccg gat ttt tat	576
Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr	
180 185 190	
aaa act aaa atc aag ctc tgc ata ctt ctt cat gct ttc aga att cgt	624
Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg	
195 200 205	
gcg gtg acc atc gat aga atg atg agt tat ctg aat tct tcc	666
Ala Val Thr Ile Asp Arg Met Met Ser Tyr Leu Asn Ser Ser	
210 215 220	

<210> 47
 <211> 222
 <212> PRT
 <213> Canis familiaris

<400> 47

Met Cys Pro Pro Arg Gly Leu Leu Leu Val Thr Ile Leu Val Leu Leu
1 5 10 15

Ser His Leu Asp His Leu Thr Trp Ala Arg Ser Leu Pro Thr Ala Ser
20 25 30

Pro Ser Pro Gly Ile Phe Gln Cys Leu Asn His Ser Gln Asn Leu Leu
35 40 45

Arg Ala Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Leu
50 55 60

Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp
65 70 75 80

Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn
85 90 95

Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser
100 105 110

Cys Leu Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu Ser
115 120 125

Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala Met
130 135 140

Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln
145 150 155 160

Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe Asn
165 170 175

Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr
180 185 190

Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg
195 200 205

Ala Val Thr Ile Asp Arg Met Met Ser Tyr Leu Asn Ser Ser
210 215 220

<210> 48
<211> 666
<212> DNA
<213> Canis familiaris

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<400> 48
ggaagaattc agataactca tcattctatc gatgggcacc gcacgaattc tgaaagcatg      60
aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggctcttcaa gggaggattt      120
ctgtggcaca gtcacactgt tgaaattcag ggccgtgaac agctcatcga tagctgtcag      180
catgttttga tccagaaaga tctgcctctt gggatccatt aaaagctttg cgttcattggc      240
cttgaattcc atctggtaca tcttcaagtc ctcatagatg ctgctaaggc acaggaccgt      300
cataaaagag gcctttccag aggccaggca actcccgtta gttatcaaag agatctctct      360
ggaagccagg caactctcat tcatgggttaa ttccagtggg aagcaggcct ccactgtgct      420
ggttttatcc tttgtgatat cttcatgac aatctcttcg gaagtgcagg aatataattc      480
tagagtttgt ctggccttct gaagcgtggt gctgacggct ctgagcaggt tttgggagtg      540
gttgaggcac tggaatatcc ctgggctcgg tgaggctgtg gggaggctcc tggcccaagt      600
aaggtggtcc aggtggctta gcaggaccag gatggtcaca aggaggaggc cgcgcggcgg      660
gcacat                                                                    666

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<210> 49
<211> 591
<212> DNA
<213> Canis familiaris

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<220>
<221> CDS
<222> (1)..(591)

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```

<400> 49
agg agc ctc ccc aca gcc tca ccg agc cca gga ata ttc cag tgc ctc      48
Arg Ser Leu Pro Thr Ala Ser Pro Ser Pro Gly Ile Phe Gln Cys Leu
1          5          10          15

aac cac tcc caa aac ctg ctg aga gcc gtc agc aac acg ctt cag aag      96
Asn His Ser Gln Asn Leu Leu Arg Ala Val Ser Asn Thr Leu Gln Lys
          20          25          30

gcc aga caa act cta gaa tta tat tcc tgc act tcc gaa gag att gat      144
Ala Arg Gln Thr Leu Glu Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp
          35          40          45

cat gaa gat atc aca aag gat aaa acc agc aca gtg gag gcc tgc tta      192
His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu
          50          55          60

cca ctg gaa tta acc atg aat gag agt tgc ctg gct tcc aga gag atc      240
Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile
65          70          75          80

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tct ttg ata act aac ggg agt tgc ctg gcc tct gga aag gcc tct ttt	288
Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe	
85 90 95	
atg acg gtc ctg tgc ctt agc agc atc tat gag gac ttg aag atg tac	336
Met Thr Val Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr	
100 105 110	
cag atg gaa ttc aag gcc atg aac gca aag ctt tta atg gat ccc aag	384
Gln Met Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys	
115 120 125	
agg cag atc ttt ctg gat caa aac atg ctg aca gct atc gat gag ctg	432
Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu	
130 135 140	
tta cag gcc ctg aat ttc aac agt gtg act gtg cca cag aaa tcc tcc	480
Leu Gln Ala Leu Asn Phe Asn Ser Val Thr Val Pro Gln Lys Ser Ser	
145 150 155 160	
ctt gaa gag ccg gat ttt tat aaa act aaa atc aag ctc tgc ata ctt	528
Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu	
165 170 175	
ctt cat gct ttc aga att cgt gcg gtg acc atc gat aga atg atg agt	576
Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asp Arg Met Met Ser	
180 185 190	
tat ctg aat tct tcc	591
Tyr Leu Asn Ser Ser	
195	

<210> 50
 <211> 197
 <212> PRT
 <213> Canis familiaris

<400> 50

Arg Ser Leu Pro Thr Ala Ser Pro Ser Pro Gly Ile Phe Gln Cys Leu	
1 5 10 15	
Asn His Ser Gln Asn Leu Leu Arg Ala Val Ser Asn Thr Leu Gln Lys	
20 25 30	
Ala Arg Gln Thr Leu Glu Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp	
35 40 45	
His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu	
50 55 60	
Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile	

65		70		75		80									
Ser	Leu	Ile	Thr	Asn	Gly	Ser	Cys	Leu	Ala	Ser	Gly	Lys	Ala	Ser	Phe
				85					90					95	
Met	Thr	Val	Leu	Cys	Leu	Ser	Ser	Ile	Tyr	Glu	Asp	Leu	Lys	Met	Tyr
			100					105					110		
Gln	Met	Glu	Phe	Lys	Ala	Met	Asn	Ala	Lys	Leu	Leu	Met	Asp	Pro	Lys
		115					120					125			
Arg	Gln	Ile	Phe	Leu	Asp	Gln	Asn	Met	Leu	Thr	Ala	Ile	Asp	Glu	Leu
	130					135					140				
Leu	Gln	Ala	Leu	Asn	Phe	Asn	Ser	Val	Thr	Val	Pro	Gln	Lys	Ser	Ser
145					150					155					160
Leu	Glu	Glu	Pro	Asp	Phe	Tyr	Lys	Thr	Lys	Ile	Lys	Leu	Cys	Ile	Leu
				165					170					175	
Leu	His	Ala	Phe	Arg	Ile	Arg	Ala	Val	Thr	Ile	Asp	Arg	Met	Met	Ser
		180						185					190		
Tyr	Leu	Asn	Ser	Ser											
		195													

<210> 51
 <211> 591
 <212> DNA
 <213> Canis familiaris

<400> 51	
ggaagaattc agataactca tcattctatc gatggtcacc gcacgaattc tgaaagcatg	60
aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggctcttcaa gggaggattt	120
ctgtggcaca gtcacactgt tgaaattcag ggcttgtaac agctcatcga tagctgtcag	180
catgttttga tccagaaaga tctgcctctt gggatccatt aaaagctttg cgttcatggc	240
cttgaattcc atctggtaca tcttcaagtc ctcatagatg ctgctaaggc acaggaccgt	300
cataaaagag gcctttccag aggccaggca actcccgtta gttatcaaag agatctctct	360
ggaagccagg caactctcat tcatggttaa ttccagtggg aagcaggcct cactgtgct	420
ggttttatcc tttgtgatat cttcatgatc aatctcttcg gaagtgcagg aatataattc	480

tagagtttgt ctggccttct gaagcgtgtt gctgacggct ctcagcaggt tttgggagtg	540
gttgaggcac tggaatatct ctgggctcgg tgaggctgtg gggaggctcc t	591

<210> 52
 <211> 921
 <212> DNA
 <213> Canis familiaris

<220>
 <221> CDS
 <222> (1)..(921)

<400> 52 ata tgg gaa ctg gag aaa gat gtt tat gtt gta gag ttg gac tgg cac Ile Trp Glu Leu Glu Lys Asp Val Tyr Val Val Glu Leu Asp Trp His 1 5 10 15	48
cct gat gcc ccc gga gaa atg gtg gtc ctc acc tgc cat acc cct gaa Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys His Thr Pro Glu 20 25 30	96
gaa gat gac atc act tgg acc tca gcg cag agc agt gaa gtc cta ggt Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln Ser Ser Glu Val Leu Gly 35 40 45	144
tct ggt aaa act ctg acc atc caa gtc aaa gaa ttt gga gat gct ggc Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly 50 55 60	192
cag tat acc tgc cat aaa gga ggc aag gtt ctg agc cgc tca ctc ctg Gln Tyr Thr Cys His Lys Gly Gly Lys Val Leu Ser Arg Ser Leu Leu 65 70 75 80	240
ttg att cac aaa aaa gaa gat gga att tgg tcc act gat atc tta aag Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys 85 90 95	288
gaa cag aaa gaa tcc aaa aat aag atc ttt ctg aaa tgt gag gca aag Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys 100 105 110	336
aat tat tct gga cgt ttc aca tgc tgg tgg ctg acg gca atc agt act Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr 115 120 125	384
gat ttg aaa ttc agt gtc aaa agt agc aga ggc ttc tct gac ccc caa Asp Leu Lys Phe Ser Val Lys Ser Ser Arg Gly Phe Ser Asp Pro Gln 130 135 140	432
ggg gtg aca tgt gga gca gtg aca ctt tca gca gag agg gtc aga gtg Gly Val Thr Cys Gly Ala Val Thr Leu Ser Ala Glu Arg Val Arg Val 145 150 155 160	480
gac aac agg gat tat aag aag tac aca gtg gag tgt cag gag ggc agt	528

Asp	Asn	Arg	Asp	Tyr	Lys	Lys	Tyr	Thr	Val	Glu	Cys	Gln	Glu	Gly	Ser		
				165					170					175			
gcc	tgc	ccc	tct	gcc	gag	gag	agc	cta	ccc	atc	gag	gtc	gtg	gtg	gat	576	
Ala	Cys	Pro	Ser	Ala	Glu	Glu	Ser	Leu	Pro	Ile	Glu	Val	Val	Val	Asp		
			180					185				190					
gct	att	cac	aag	ctc	aag	tat	gaa	aac	tac	acc	agc	agc	ttc	ttc	atc	624	
Ala	Ile	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr	Thr	Ser	Ser	Phe	Phe	Ile		
		195					200					205					
aga	gac	atc	atc	aaa	cca	gac	cca	ccc	aca	aac	ctg	cag	ctg	aag	cca	672	
Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Thr	Asn	Leu	Gln	Leu	Lys	Pro		
	210					215					220						
ttg	aaa	aat	tct	cgg	cac	gtg	gag	gtc	agc	tgg	gaa	tac	ccc	gac	acc	720	
Leu	Lys	Asn	Ser	Arg	His	Val	Glu	Val	Ser	Trp	Glu	Tyr	Pro	Asp	Thr		
225				230					235					240			
tgg	agc	acc	cca	cat	tcc	tac	ttc	tcc	ctg	aca	ttt	tgc	ata	cag	gcc	768	
Trp	Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu	Thr	Phe	Cys	Ile	Gln	Ala		
			245					250					255				
cag	ggc	aag	aac	aat	aga	gaa	aag	aaa	gat	aga	ctc	tgc	gtg	gac	aag	816	
Gln	Gly	Lys	Asn	Asn	Arg	Glu	Lys	Lys	Asp	Arg	Leu	Cys	Val	Asp	Lys		
			260					265				270					
acc	tca	gcc	aag	gtc	gtg	tgc	cac	aag	gat	gcc	aag	atc	cgc	gtg	caa	864	
Thr	Ser	Ala	Lys	Val	Val	Cys	His	Lys	Asp	Ala	Lys	Ile	Arg	Val	Gln		
		275					280					285					
gcc	cga	gac	cgc	tac	tat	agt	tca	tcc	tgg	agc	gac	tgg	gca	tct	gtg	912	
Ala	Arg	Asp	Arg	Tyr	Tyr	Ser	Ser	Ser	Trp	Ser	Asp	Trp	Ala	Ser	Val		
	290					295					300						
tcc	tgc	agt														921	
Ser	Cys	Ser															
305																	

<210> 53
 <211> 307
 <212> PRT
 <213> Canis familiaris

<400> 53

Ile	Trp	Glu	Leu	Glu	Lys	Asp	Val	Tyr	Val	Val	Glu	Leu	Asp	Trp	His
1				5				10					15		

Pro	Asp	Ala	Pro	Gly	Glu	Met	Val	Val	Leu	Thr	Cys	His	Thr	Pro	Glu
		20					25					30			

Glu	Asp	Asp	Ile	Thr	Trp	Thr	Ser	Ala	Gln	Ser	Ser	Glu	Val	Leu	Gly
	35						40					45			

Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly
 50 55 60

Gln Tyr Thr Cys His Lys Gly Gly Lys Val Leu Ser Arg Ser Leu Leu
 65 70 75 80

Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys
 85 90 95

Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys
 100 105 110

Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr
 115 120 125

Asp Leu Lys Phe Ser Val Lys Ser Ser Arg Gly Phe Ser Asp Pro Gln
 130 135 140

Gly Val Thr Cys Gly Ala Val Thr Leu Ser Ala Glu Arg Val Arg Val
 145 150 155 160

Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser
 165 170 175

Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp
 180 185 190

Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile
 195 200 205

Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr Asn Leu Gln Leu Lys Pro
 210 215 220

Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr
 225 230 235 240

Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Ile Gln Ala
 245 250 255

Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Cys Val Asp Lys
 260 265 270

Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln
 275 280 285

Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asp Trp Ala Ser Val
 290 295 300

Ser Cys Ser
 305

<210> 54
 <211> 921
 <212> DNA
 <213> Canis familiaris

<400> 54
 actgcaggac acagatgccc agtcgctcca ggatgaacta tagtagcggg ctcgggcttg 60
 cacgcggatc ttggcaccct tgtggcacac gaccttggct gaggtcttgt ccacgcagag 120
 tctatctttc ttttctctat tgttcttgcc ctgggcttgt atgcaaatg tcagggagaa 180
 gtaggaatgt ggggtgctcc aggtgtcggg gtattcccag ctgacctcca cgtgccgaga 240
 atttttcaat ggcttcagct gcaggtttgt ggggtgggtct ggtttgatga tgtctctgat 300
 gaagaagctg ctggtgtagt tttcatactt gagcttgtga atagcatcca ccacgacctc 360
 gatgggtagg ctctctcctg cagaggggca ggcactgccc tcttgacact ccactgtgta 420
 cttcttataa tccctgttgt ccactctgac cctctctgct gaaagtgtca ctgctccaca 480
 tgtcaccctt tgggggtcag agaagcctct gctacttttg aactgaatt tcaaatcagt 540
 actgattgcc gtcagccacc agcatgtgaa acgtccagaa taattctttg cctcacattt 600
 cagaaagatc ttatttttgg attctttctg ttcctttaag atatcagtgg accaaattcc 660
 atcttctttt ttgtgaatca acaggagtga gcggtcaga accttgctc ctttatggca 720
 ggtatactgg ccagcatctc caaattcttt gacttggatg gtcagagttt taccagaacc 780
 taggacttca ctgctctgcg ctgagggtcca agtgatgtca tcttcttcag gggtatggca 840
 ggtgaggacc accatttctc cgggggcatc aggggtgccag tccaactcta caacataaac 900
 atctttctcc agttcccata t 921

<210> 55
 <211> 985
 <212> DNA
 <213> Felis catus

<220>
 <221> CDS
 <222> (1)..(984)

<400> 55
 atg cat cct cag cag ttg gtc atc gcc tgg ttt tcc ctg gtt ttg ctg 48
 Met His Pro Gln Gln Leu Val Ile Ala Trp Phe Ser Leu Val Leu Leu
 1 5 10 15
 gca cct ccc ctc atg gcc ata tgg gaa ctg gag aaa aac gtt tat gtt 96
 Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val
 20 25 30
 gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctc 144
 Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
 35 40 45
 acc tgc aat act cct gaa gaa gat gac atc acc tgg acc tct gac cag 192
 Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln
 50 55 60
 agc agt gaa gtc cta ggc tct ggt aaa act ctg acc atc caa gtc aaa 240
 Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
 65 70 75 80
 gaa ttt gca gat gct ggc cag tat acc tgt cat aaa gga ggc gag gtt 288
 Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
 85 90 95
 ctg agc cat tcg ttc ctc ctg ata cac aaa aag gaa gat gga att tgg 336
 Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
 100 105 110
 tcc act gat atc tta agg gaa cag aaa gaa tcc aaa aat aag atc ttt 384
 Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
 115 120 125
 cta aaa tgt gag gca aag aat tat tct gga cgt ttc acc tgc tgg tgg 432
 Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
 130 135 140
 ctg acg gca atc agt acc gat ttg aaa ttc act gtc aaa agc agc aga 480
 Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg
 145 150 155 160
 ggc tcc tct gac ccc caa ggg gtg act tgt gga gca gcg aca ctc tca 528
 Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser
 165 170 175
 gca gag aag gtc aga gtg gac aac agg gat tat aag aag tac aca gtg 576
 Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
 180 185 190
 gag tgt cag gag ggc agt gcc tgc ccg gct gcc gag gag agc cta ccc 624
 Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro
 195 200 205

att gaa gtc gtg gtg gac gct att cac aag ctc aag tac gaa aac tac	672
Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr	
210 215 220	
acc agc agc ttc ttc atc agg gac atc atc aaa ccg gac cca ccc aag	720
Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys	
225 230 235 240	
aac ctg caa ctg aag cca tta aaa aat tct cgg cat gtg gaa gtg agc	768
Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser	
245 250 255	
tgg gaa tac cct gac acc tgg agc acc cca cat tcc tac ttc tcc tta	816
Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu	
260 265 270	
aca ttt ggc gta cag gtc cag ggc aag aac aac aga gaa aag aaa gac	864
Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp	
275 280 285	
aga ctc tcc gtg gac aag acc tca gcc aag gtc gtg tgc cac aag gat	912
Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp	
290 295 300	
gcc aag atc cgc gtg caa gcc aga gac cgc tac tat agc tca tcc tgg	960
Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp	
305 310 315 320	
agc aac tgg gca tcc gtg tcc tgc a	985
Ser Asn Trp Ala Ser Val Ser Cys	
325	

<210> 56
 <211> 328
 <212> PRT
 <213> Felis catus

<400> 56

Met His Pro Gln Gln Leu Val Ile Ala Trp Phe Ser Leu Val Leu Leu	
1 5 10 15	
Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val	
20 25 30	
Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu	
35 40 45	
Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln	
50 55 60	

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
 65 70 75 80
 Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
 85 90 95
 Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
 100 105 110
 Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
 115 120 125
 Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
 130 135 140
 Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg
 145 150 155 160
 Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser
 165 170 175
 Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
 180 185 190
 Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro
 195 200 205
 Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
 210 215 220
 Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys
 225 230 235 240
 Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
 245 250 255
 Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
 260 265 270
 Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
 275 280 285
 Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp

290

295

300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
 305 310 315 320

Ser Asn Trp Ala Ser Val Ser Cys
 325

<210> 57
 <211> 985
 <212> DNA
 <213> Felis catus

<400> 57
 tgcaggacac ggatgccag ttgctccagg atgagctata gtagcggctct ctggcttgca 60
 cgcggatctt ggcatacctt tggcacacga ccttggtctga ggtcttgtcc acggagagtc 120
 tgtctttctt ttctctgttg ttcttgcctt ggacctgtac gccaaatgtt aaggagaagt 180
 aggaatgtgg ggtgctccag gtgtcagggt attcccagct cacttccaca tgccgagaat 240
 tttttaatgg cttcagttgc aggttcttgg gtgggtccgg tttgatgatg tccctgatga 300
 agaagctgct ggtgtagttt tcgtacttga gcttgtgaat agcgtccacc acgacttcaa 360
 tgggtaggct ctctcggca gccgggcagg cactgcctc ctgacactcc actgtgtact 420
 tcttataatc cctgttgtcc actctgacct tctctgctga gagtgtcgt gctccacaag 480
 tcaccccttg ggggtcagag gagcctctgc tgcttttgac agtgaatttc aaatcgggtac 540
 tgattgccgt cagccaccag caggtgaaac gtccagaata attctttgcc tcacatttta 600
 gaaagatctt atttttggat tctttctgtt cccttaagat atcagtggac caaattccat 660
 cttccttttt gtgtatcagg aggaacgaat ggctcagaac ctgcctcctt ttatgacagg 720
 tatactggcc agcatctgca aattctttga cttggatggt cagagtttta ccagagccta 780
 ggacttcact gctctgggtc gaggtccagg tgatgtcatc ttcttcagga gtattgcagg 840
 tgaggaccac catttctccg ggggcacag ggtgccagtc caactctaca acataaacgt 900
 ttttctccag ttcccatatg gccatgaggg gaggtgccag caaaaccagg gaaaaccagg 960
 cgatgaccaa ctgctgagga tgcatt 985

<210> 58
 <211> 987
 <212> DNA
 <213> Canis familiaris

<220>
 <221> CDS
 <222> (1)..(987)

<400> 58

atg cac cct cag cag ttg gtc atc tcc tgg ttt tcc ctc gtt ttg ctg	48
Met His Pro Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Leu Leu	
1 5 10 15	
gcg tct ccc ctc atg gcc ata tgg gaa ctg gag aaa gat gtt tat gtt	96
Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asp Val Tyr Val	
20 25 30	
gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctc	144
Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu	
35 40 45	
acc tgc cat acc cct gaa gaa gat gac atc act tgg acc tca gcg cag	192
Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln	
50 55 60	
agc agt gaa gtc cta ggt tct ggt aaa act ctg acc atc caa gtc aaa	240
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys	
65 70 75 80	
gaa ttt gga gat gct ggc cag tat acc tgc cat aaa gga ggc aag gtt	288
Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val	
85 90 95	
ctg agc cgc tca ctc ctg ttg att cac aaa aaa gaa gat gga att tgg	336
Leu Ser Arg Ser Leu Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp	
100 105 110	
tcc act gat atc tta aag gaa cag aaa gaa tcc aaa aat aag atc ttt	384
Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe	
115 120 125	
ctg aaa tgt gag gca aag aat tat tct gga cgt ttc aca tgc tgg tgg	432
Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp	
130 135 140	
ctg acg gca atc agt act gat ttg aaa ttc agt gtc aaa agt agc aga	480
Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg	
145 150 155 160	
ggc ttc tct gac ccc caa ggg gtg aca tgt gga gca gtg aca ctt tca	528
Gly Phe Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser	
165 170 175	
gca gag agg gtc aga gtg gac aac agg gat tat aag aag tac aca gtg	576
Ala Glu Arg Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val	
180 185 190	
gag tgt cag gag ggc agt gcc tgc ccc tct gcc gag gag agc cta ccc	624
Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro	
195 200 205	

atc gag gtc gtg gtg gat gct att cac aag ctc aag tat gaa aac tac	672
Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr	
210 215 220	
acc agc agc ttc ttc atc aga gac atc atc aaa cca gac cca ccc aca	720
Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr	
225 230 235 240	
aac ctg cag ctg aag cca ttg aaa aat tct cgg cac gtg gag gtc agc	768
Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser	
245 250 255	
tgg gaa tac ccc gac acc tgg agc acc cca cat tcc tac ttc tcc ctg	816
Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu	
260 265 270	
aca ttt tgc ata cag gcc cag ggc aag aac aat aga gaa aag aaa gat	864
Thr Phe Cys Ile Gln Ala Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp	
275 280 285	
aga ctc tgc gtg gac aag acc tca gcc aag gtc gtg tgc cac aag gat	912
Arg Leu Cys Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp	
290 295 300	
gcc aag atc cgc gtg caa gcc cga gac cgc tac tat agt tca tcc tgg	960
Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp	
305 310 315 320	
agc gac tgg gca tct gtg tca tgc agt	987
Ser Asp Trp Ala Ser Val Ser Cys Ser	
325	

<210> 59
 <211> 329
 <212> PRT
 <213> Canis familiaris

<400> 59

Met His Pro Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Leu Leu	
1 5 10 15	
Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asp Val Tyr Val	
20 25 30	
Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu	
35 40 45	
Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln	
50 55 60	

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
 65 70 75 80
 Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val
 85 90 95
 Leu Ser Arg Ser Leu Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
 100 105 110
 Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
 115 120 125
 Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
 130 135 140
 Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg
 145 150 155 160
 Gly Phe Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser
 165 170 175
 Ala Glu Arg Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
 180 185 190
 Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro
 195 200 205
 Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
 210 215 220
 Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr
 225 230 235 240
 Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
 245 250 255
 Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
 260 265 270
 Thr Phe Cys Ile Gln Ala Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
 275 280 285
 Arg Leu Cys Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp

290

295

300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
 305 310 315 320

Ser Asp Trp Ala Ser Val Ser Cys Ser
 325

<210> 60
 <211> 987
 <212> DNA
 <213> Canis familiaris

<400> 60
 actgcatgac acagatgccc agtcgctcca ggatgaacta tagtagcggc ctcgggcttg 60
 cacgcggtac ttggcatcct tgtggcacac gaccttggct gaggtcctgt ccacgcagag 120
 tctatctttc ttttctctat tgttcttgcc ctgggcctgt atgcaaatg tcagggagaa 180
 gtaggaatgt ggggtgctcc aggtgtcggg gtattcccag ctgacctcca cgtgccgaga 240
 atttttcaat ggcttcagct gcagggttct ggggtgggtct ggtttgatga tgtctctgat 300
 gaagaagctg ctggtgtagt tttcatactt gagcttgtga atagcatcca ccacgacctc 360
 gatgggtagg ctctcctcgg cagaggggca ggcactgccc tctgacact ccactgtgta 420
 cttcttataa tccctgttct ccactctgac cctctctgct gaaagtgtca ctgctccaca 480
 tgtcaccctt tgggggtcag agaagcctct gctacttttg aactgaatt tcaaatcagt 540
 actgattgcc gtcagccacc agcatgtgaa acgtccagaa taattctttg cctcacattt 600
 cagaaagatc ttatttttgg attctttctg ttcctttaag atatcagtgg accaaattcc 660
 atcttctttt ttgtgaatca acaggagtga gcggtcaga accttgctc ctttatggca 720
 ggtatactgg ccagcatctc caaattcttt gacttggatg gtcagagttt taccagaacc 780
 taggacttca ctgctctgcg ctgagggtcca agtgatgtca tcttcttcag gggtatggca 840
 ggtgaggacc accatttctc cgggggcac aggggtgccag tccaactcta caacataaac 900
 atctttctcc agttcccata tggccatgag gggagacgcc agcaaacga gggaaaacca 960
 ggagatgacc aactgctgag ggtgcat 987

<210> 61
 <211> 1599
 <212> DNA
 <213> Canis familiaris

<220>
 <221> CDS
 <222> (1)..(1599)

<400> 61

atg cac cct cag cag ttg gtc atc tcc tgg ttt tcc ctc gtt ttg ctg	48
Met His Pro Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Leu Leu	
1 5 10 15	
gcg tct ccc ctc atg gcc ata tgg gaa ctg gag aaa gat gtt tat gtt	96
Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asp Val Tyr Val	
20 25 30	
gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctc	144
Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu	
35 40 45	
acc tgc cat acc cct gaa gaa gat gac atc act tgg acc tca gcg cag	192
Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln	
50 55 60	
agc agt gaa gtc cta ggt tct ggt aaa act ctg acc atc caa gtc aaa	240
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys	
65 70 75 80	
gaa ttt gga gat gct ggc cag tat acc tgc cat aaa gga ggc aag gtt	288
Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val	
85 90 95	
ctg agc cgc tca ctc ctg ttg att cac aaa aaa gaa gat gga att tgg	336
Leu Ser Arg Ser Leu Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp	
100 105 110	
tcc act gat atc tta aag gaa cag aaa gaa tcc aaa aat aag atc ttt	384
Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe	
115 120 125	
ctg aaa tgt gag gca aag aat tat tct gga cgt ttc aca tgc tgg tgg	432
Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp	
130 135 140	
ctg acg gca atc agt act gat ttg aaa ttc agt gtc aaa agt agc aga	480
Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg	
145 150 155 160	
ggc ttc tct gac ccc caa ggg gtg aca tgt gga gca gtg aca ctt tca	528
Gly Phe Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser	
165 170 175	
gca gag agg gtc aga gtg gac aac agg gat tat aag aag tac aca gtg	576
Ala Glu Arg Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val	
180 185 190	
gag tgt cag gag ggc agt gcc tgc ccc tct gcc gag gag agc cta ccc	624
Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro	
195 200 205	

atc gag gtc gtg gtg gat gct att cac aag ctc aag tat gaa aac tac Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr 210 215 220	672
acc agc agc ttc ttc atc aga gac atc atc aaa cca gac cca ccc aca Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr 225 230 235 240	720
aac ctg cag ctg aag cca ttg aaa aat tct cgg cac gtg gag gtc agc Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser 245 250 255	768
tgg gaa tac ccc gac acc tgg agc acc cca cat tcc tac ttc tcc ctg Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu 260 265 270	816
aca ttt tgc ata cag gcc cag ggc aag aac aat aga gaa aag aaa gat Thr Phe Cys Ile Gln Ala Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp 275 280 285	864
aga ctc tgc gtg gac aag acc tca gcc aag gtc gtg tgc cac aag gat Arg Leu Cys Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp 290 295 300	912
gcc aag atc cgc gtg caa gcc cga gac cgc tac tat agt tca tcc tgg Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp 305 310 315 320	960
agc gac tgg gca tct gtg tca tgc agt ggt ggc ggt ggc ggc gga tct Ser Asp Trp Ala Ser Val Ser Cys Ser Gly Gly Gly Gly Gly Gly Ser 325 330 335	1008
aga aac ttg cca acc cct act cca tcc ccg ggt atg ttc caa tgt ttg Arg Asn Leu Pro Thr Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu 340 345 350	1056
aac cac tcc caa acc ttg ttg aga gcc gtc agc aac acg ctt cag aag Asn His Ser Gln Thr Leu Leu Arg Ala Val Ser Asn Thr Leu Gln Lys 355 360 365	1104
gcc aga caa act cta gaa tta tat tcc tgc act tcc gaa gag att gat Ala Arg Gln Thr Leu Glu Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp 370 375 380	1152
cat gaa gat atc aca aag gat aaa acc agc aca gtg gag gcc tgc tta His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu 385 390 395 400	1200
cca ctg gaa tta acc atg aat gag agt tgc ctg gct tcc aga gag atc Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile 405 410 415	1248
tct ttg ata act aac ggg agt tgc ctg gcc tct gga aag gcc tct ttt Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe 420 425 430	1296

atg acg gtc ctg tgc ctt agc agc atc tat gag gac ttg aag atg tac	1344
Met Thr Val Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr	
435 440 445	
cag atg gaa ttc aag gcc atg aac gca aag ctt tta atg gat ccc aag	1392
Gln Met Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys	
450 455 460	
agg cag atc ttt ctg gat caa aac atg ctg aca gct atc gat gag ctg	1440
Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu	
465 470 475 480	
tta cag gcc ctg aat ttc aac agt gtg act gtg cca cag aaa tcc tcc	1488
Leu Gln Ala Leu Asn Phe Asn Ser Val Thr Val Pro Gln Lys Ser Ser	
485 490 495	
ctt gaa gag ccg gat ttt tat aaa act aaa atc aag ctc tgc ata ctt	1536
Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu	
500 505 510	
ctt cat gct ttc aga att cgt gcg gtg acc atc aat aga atg atg tcc	1584
Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser	
515 520 525	
tac ttg aac tct tcc	1599
Tyr Leu Asn Ser Ser	
530	

<210> 62
 <211> 533
 <212> PRT
 <213> Canis familiaris

<400> 62

Met His Pro Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Leu Leu	
1 5 10 15	
Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asp Val Tyr Val	
20 25 30	
Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu	
35 40 45	
Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln	
50 55 60	
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys	
65 70 75 80	
Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val	

85	90	95
Leu Ser Arg Ser Leu Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp		
100	105	110
Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe		
115	120	125
Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp		
130	135	140
Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg		
145	150	155
Gly Phe Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser		
165	170	175
Ala Glu Arg Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val		
180	185	190
Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro		
195	200	205
Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr		
210	215	220
Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr		
225	230	235
Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser		
245	250	255
Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu		
260	265	270
Thr Phe Cys Ile Gln Ala Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp		
275	280	285
Arg Leu Cys Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp		
290	295	300
Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp		
305	310	315
		320

Ser Asp Trp Ala Ser Val Ser Cys Ser Gly Gly Gly Gly Gly Gly Ser
325 330 335

Arg Asn Leu Pro Thr Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu
340 345 350

Asn His Ser Gln Thr Leu Leu Arg Ala Val Ser Asn Thr Leu Gln Lys
355 360 365

Ala Arg Gln Thr Leu Glu Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp
370 375 380

His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu
385 390 395 400

Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile
405 410 415

Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe
420 425 430

Met Thr Val Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr
435 440 445

Gln Met Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys
450 455 460

Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu
465 470 475 480

Leu Gln Ala Leu Asn Phe Asn Ser Val Thr Val Pro Gln Lys Ser Ser
485 490 495

Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu
500 505 510

Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser
515 520 525

Tyr Leu Asn Ser Ser
530

<210> 63
 <211> 1599
 <212> DNA
 <213> Canis familiaris

<400> 63
 ggaagagttc aagtaggaca tcattctatt gatggtcacc gcacgaattc tgaaagcatg 60
 aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggctcttcaa gggaggattt 120
 ctgtggcaca gtcacactgt tgaaattcag ggctgtaac agctcatcga tagctgtcag 180
 catgttttga tccagaaaga tctgcctctt gggatccatt aaaagctttg cgttcatggc 240
 cttgaattcc atctggtaca tcttcaagtc ctcatagatg ctgctaaggc acaggaccgt 300
 cataaaagag gcctttccag aggccaggca actcccgtta gttatcaaag agatctctct 360
 ggaagccagg caactctcat tcatggttaa ttccagtggc aagcaggcct ccactgtgct 420
 ggttttatcc tttgtgatat cttcatgac aatctcttcg gaagtgcagg aatataattc 480
 tagagtttgt ctggccttct gaagcgtggt gctgacggct ctcaacaagg tttgggagtg 540
 gttcaaacat tggaacatac ccggggatgg agtaggggtt ggcaagtttc tagatccgcc 600
 gccaccgcca ccactgcatg acacagatgc ccagtcgctc caggatgaac tatagtagcg 660
 gtctcgggct tgcacgcgga tcttggcatc cttgtggcac acgaccttgg ctgaggtctt 720
 gtccacgcag agtctatctt tcttttctct attgttcttg ccctgggcct gtatgcaaaa 780
 tgtcagggag aagtaggaat gtggggtgct ccagggtgctg gggatttccc agctgacctc 840
 cacgtgccga gaatttttca atggcttcag ctgcagggtt gtgggtgggt ctggtttgat 900
 gatgtctctg atgaagaagc tgctgggtgta gttttcatac ttgagcttgt gaatagcatc 960
 caccacgacc tcgatgggta ggctctctc ggcagagggg caggcactgc cctcctgaca 1020
 ctccactgtg tacttcttat aatccctggt gtccactctg accctctctg ctgaaagtgt 1080
 cactgctcca catgtcacc cttgggggtc agagaagcct ctgctacttt tgacactgaa 1140
 tttcaaatca gtactgattg ccgtcagcca ccagcatgtg aaacgtccag aataattctt 1200
 tgccctcatat ttcagaaaga tcttattttt ggattctttc tgttccttta agatatcagt 1260
 ggaccaaatt ccatcttctt ttttgtgaat caacaggagt gagcggctca gaaccttgcc 1320
 tcctttatgg caggtatact ggccagcatc tccaaattct ttgacttgga tggtcagagt 1380
 tttaccagaa cctaggactt cactgctctg cgctgaggtc caagtgatgt catcttcttc 1440
 aggggtatgg caggtgagga ccaccatttc tccgggggca tcagggtgcc agtccaactc 1500

tacaacataa acatctttct ccagttccca tatggccatg aggggagacg ccagcaaaac 1560
gagggaaaac caggagatga ccaactgctg aggggtgcat 1599

<210> 64
<211> 0
<212> DNA
<213> Canis familiaris

<400> 64
000

<210> 65
<211> 0
<212> DNA
<213> Canis familiaris

<400> 65
000

<210> 66
<211> 1533
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (1)..(1533)

<400> 66
ata tgg gaa ctg gag aaa gat gtt tat gtt gta gag ttg gac tgg cac 48
Ile Trp Glu Leu Glu Lys Asp Val Tyr Val Val Glu Leu Asp Trp His
1 5 10 15
cct gat gcc ccc gga gaa atg gtg gtc ctc acc tgc cat acc cct gaa 96
Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys His Thr Pro Glu
20 25 30
gaa gat gac atc act tgg acc tca gcg cag agc agt gaa gtc cta ggt 144
Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln Ser Ser Glu Val Leu Gly
35 40 45
tct ggt aaa act ctg acc atc caa gtc aaa gaa ttt gga gat gct ggc 192
Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly
50 55 60
cag tat acc tgc cat aaa gga ggc aag gtt ctg agc cgc tca ctc ctg 240
Gln Tyr Thr Cys His Lys Gly Gly Lys Val Leu Ser Arg Ser Leu Leu
65 70 75 80
ttg att cac aaa aaa gaa gat gga att tgg tcc act gat atc tta aag 288
Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys
85 90 95
gaa cag aaa gaa tcc aaa aat aag atc ttt ctg aaa tgt gag gca aag 336

Glu	Gln	Lys	Glu	Ser	Lys	Asn	Lys	Ile	Phe	Leu	Lys	Cys	Glu	Ala	Lys	
			100					105					110			
aat	tat	tct	gga	cgt	ttc	aca	tgc	tgg	tgg	ctg	acg	gca	atc	agt	act	384
Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Trp	Trp	Leu	Thr	Ala	Ile	Ser	Thr	
		115					120					125				
gat	ttg	aaa	ttc	agt	gtc	aaa	agt	agc	aga	ggc	ttc	tct	gac	ccc	caa	432
Asp	Leu	Lys	Phe	Ser	Val	Lys	Ser	Ser	Arg	Gly	Phe	Ser	Asp	Pro	Gln	
	130					135					140					
ggg	gtg	aca	tgt	gga	gca	gtg	aca	ctt	tca	gca	gag	agg	gtc	aga	gtg	480
Gly	Val	Thr	Cys	Gly	Ala	Val	Thr	Leu	Ser	Ala	Glu	Arg	Val	Arg	Val	
145					150					155					160	
gac	aac	agg	gat	tat	aag	aag	tac	aca	gtg	gag	tgt	cag	gag	ggc	agt	528
Asp	Asn	Arg	Asp	Tyr	Lys	Lys	Tyr	Thr	Val	Glu	Cys	Gln	Glu	Gly	Ser	
				165				170						175		
gcc	tgc	ccc	tct	gcc	gag	gag	agc	cta	ccc	atc	gag	gtc	gtg	gtg	gat	576
Ala	Cys	Pro	Ser	Ala	Glu	Glu	Ser	Leu	Pro	Ile	Glu	Val	Val	Val	Asp	
			180					185					190			
gct	att	cac	aag	ctc	aag	tat	gaa	aac	tac	acc	agc	agc	ttc	ttc	atc	624
Ala	Ile	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr	Thr	Ser	Ser	Phe	Phe	Ile	
		195					200					205				
aga	gac	atc	atc	aaa	cca	gac	cca	ccc	aca	aac	ctg	cag	ctg	aag	cca	672
Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Thr	Asn	Leu	Gln	Leu	Lys	Pro	
	210					215					220					
ttg	aaa	aat	tct	cgg	cac	gtg	gag	gtc	agc	tgg	gaa	tac	ccc	gac	acc	720
Leu	Lys	Asn	Ser	Arg	His	Val	Glu	Val	Ser	Trp	Glu	Tyr	Pro	Asp	Thr	
225					230					235					240	
tgg	agc	acc	cca	cat	tcc	tac	ttc	tcc	ctg	aca	ttt	tgc	ata	cag	gcc	768
Trp	Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu	Thr	Phe	Cys	Ile	Gln	Ala	
				245					250					255		
cag	ggc	aag	aac	aat	aga	gaa	aag	aaa	gat	aga	ctc	tgc	gtg	gac	aag	816
Gln	Gly	Lys	Asn	Asn	Arg	Glu	Lys	Lys	Asp	Arg	Leu	Cys	Val	Asp	Lys	
			260					265					270			
acc	tca	gcc	aag	gtc	gtg	tgc	cac	aag	gat	gcc	aag	atc	cgc	gtg	caa	864
Thr	Ser	Ala	Lys	Val	Val	Cys	His	Lys	Asp	Ala	Lys	Ile	Arg	Val	Gln	
		275					280					285				
gcc	cga	gac	cgc	tac	tat	agt	tca	tcc	tgg	agc	gac	tgg	gca	tct	gtg	912
Ala	Arg	Asp	Arg	Tyr	Tyr	Ser	Ser	Ser	Trp	Ser	Asp	Trp	Ala	Ser	Val	
	290					295					300					
tca	tgc	agt	ggt	ggc	ggt	ggc	ggc	gga	tct	aga	aac	ttg	cca	acc	cct	960
Ser	Cys	Ser	Gly	Gly	Gly	Gly	Gly	Gly	Ser	Arg	Asn	Leu	Pro	Thr	Pro	
305					310				315						320	
act	cca	tcc	ccg	ggt	atg	ttc	caa	tgt	ttg	aac	cac	tcc	caa	acc	ttg	1008
Thr	Pro	Ser	Pro	Gly	Met	Phe	Gln	Cys	Leu	Asn	His	Ser	Gln	Thr	Leu	

	325	330	335	
ttg aga gcc gtc agc aac acg ctt cag aag gcc aga caa act cta gaa				1056
Leu Arg Ala Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu				
	340	345	350	
tta tat tcc tgc act tcc gaa gag att gat cat gaa gat atc aca aag				1104
Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys				
	355	360	365	
gat aaa acc agc aca gtg gag gcc tgc tta cca ctg gaa tta acc atg				1152
Asp Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met				
	370	375	380	
aat gag agt tgc ctg gct tcc aga gag atc tct ttg ata act aac ggg				1200
Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly				
	385	390	395	400
agt tgc ctg gcc tct gga aag gcc tct ttt atg acg gtc ctg tgc ctt				1248
Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu				
	405	410	415	
agc agc atc tat gag gac ttg aag atg tac cag atg gaa ttc aag gcc				1296
Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala				
	420	425	430	
atg aac gca aag ctt tta atg gat ccc aag agg cag atc ttt ctg gat				1344
Met Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp				
	435	440	445	
caa aac atg ctg aca gct atc gat gag ctg tta cag gcc ctg aat ttc				1392
Gln Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe				
	450	455	460	
aac agt gtg act gtg cca cag aaa tcc tcc ctt gaa gag ccg gat ttt				1440
Asn Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe				
	465	470	475	480
tat aaa act aaa atc aag ctc tgc ata ctt ctt cat gct ttc aga att				1488
Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile				
	485	490	495	
cgt gcg gtg acc atc aat aga atg atg tcc tac ttg aac tct tcc				1533
Arg Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ser Ser				
	500	505	510	

<210> 67
 <211> 511
 <212> PRT
 <213> Canis familiaris

<400> 67

Ile Trp Glu Leu Glu Lys Asp Val Tyr Val Val Glu Leu Asp Trp His
1 5 10 15

Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys His Thr Pro Glu
 20 25 30

Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln Ser Ser Glu Val Leu Gly
 35 40 45

Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly
 50 55 60

Gln Tyr Thr Cys His Lys Gly Gly Lys Val Leu Ser Arg Ser Leu Leu
 65 70 75 80

Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys
 85 90 95

Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys
 100 105 110

Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr
 115 120 125

Asp Leu Lys Phe Ser Val Lys Ser Ser Arg Gly Phe Ser Asp Pro Gln
 130 135 140

Gly Val Thr Cys Gly Ala Val Thr Leu Ser Ala Glu Arg Val Arg Val
 145 150 155 160

Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser
 165 170 175

Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp
 180 185 190

Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile
 195 200 205

Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr Asn Leu Gln Leu Lys Pro
 210 215 220

Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr
 225 230 235 240

Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Ile Gln Ala
 245 250 255
 Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Cys Val Asp Lys
 260 265 270
 Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln
 275 280 285
 Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asp Trp Ala Ser Val
 290 295 300
 Ser Cys Ser Gly Gly Gly Gly Gly Gly Ser Arg Asn Leu Pro Thr Pro
 305 310 315 320
 Thr Pro Ser Pro Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu
 325 330 335
 Leu Arg Ala Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu
 340 345 350
 Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys
 355 360 365
 Asp Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met
 370 375 380
 Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly
 385 390 395 400
 Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu
 405 410 415
 Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala
 420 425 430
 Met Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp
 435 440 445
 Gln Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe
 450 455 460
 Asn Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe

465 470 475 480

Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile
485 490 495

Arg Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ser Ser
500 505 510

<210> 68
<211> 1533
<212> DNA
<213> Canis familiaris

<400> 68
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aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggctcttcaa gggaggattt 120
ctgtggcaca gtcacactgt tgaaattcag ggctgtaac agctcatcga tagctgtcag 180
catgttttga tccagaaaga tctgcctctt gggatccatt aaaagctttg cgttcatggc 240
cttgaattcc atctgttaca tcttcaagtc ctcatagatg ctgctaaggc acaggaccgt 300
cataaaagag gcctttccag aggccaggca actcccgtta gttatcaaag agatctctct 360
ggaagccagg caactctcat tcatggttaa ttccagtggg aagcaggcct cactgtgct 420
ggttttatcc tttgtgatat cttcatgac aatctcttcg gaagtgcagg aatataattc 480
tagagtttgt ctggccttct gaagcgtggt gctgacggct ctcaacaagg tttgggagtg 540
gttcaaacat tggaacatac ccggggatgg agtaggggtt ggcaagtttc tagatccgcc 600
gccaccgcca cactgcatg acacagatgc ccagtcgctc caggatgaac tatagtagcg 660
gtctcgggct tgcacgcgga tcttggcatc cttgtggcac acgaccttgg ctgaggtctt 720
gtccacgcag agtctatctt tcttttctct attgttcttg ccctgggcct gtatgcaaaa 780
tgtcagggag aagtaggaat gtgggggtgct ccaggtgtcg gggattccc agctgacctc 840
cacgtgccga gaatttttca atggcttcag ctgcagggtt gtgggtgggt ctggtttgat 900
gatgtctctg atgaagaagc tgctgggtgta gttttcatac ttgagcttgt gaatagcatc 960
caccacgacc tcgatgggta ggctctctc gccagagggg caggcactgc cctcctgaca 1020
ctccactgtg tacttcttat aatccctggt gtccactctg accctctctg ctgaaagtgt 1080
cactgctcca catgtcacc cttgggggtc agagaagcct ctgctacttt tgacactgaa 1140
tttcaaatca gtactgattg ccgtcagcca ccagcatgtg aaacgtccag aataattctt 1200

tgcctcacat ttcagaaaga tcttattttt ggattctttc tgttccttta agatatcagt 1260
 ggaccaaatt ccatcttctt ttttgtgaat caacaggagt gagcggtca gaaccttgcc 1320
 tccttttatgg caggtatact ggccagcacc tccaaattct ttgacttgga tggtcagagt 1380
 tttaccagaa cctaggactt cactgctctg cgctgaggtc caagtgatgt catcttcttc 1440
 aggggtatgg caggtgagga ccaccatttc tccgggggca tcagggtgcc agtccaactc 1500
 tacaacataa acatctttct ccagttccca tat 1533

<210> 69
 <211> 30
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic Primer

<400> 69
 gccaaagctcg aaattaaccc tcactaaagg 30

<210> 70
 <211> 28
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic Primer

<400> 70
 cgacggccag tgaattgtaa tacgactc 28

<210> 71
 <211> 31
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic Primer

<400> 71
 agtgatgaag gcctggaatc agattacttt g 31

<210> 72
 <211> 32
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic Primer

<400> 72
 atggcctgga acacttctct gaaagaatat ga 32

<210> 73
 <211> 30
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic Primer

<400> 73
 aactattgag cacagggata aagatgactg 30

<210> 74
 <211> 33
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic Primer

<400> 74
 aatatctaatt tcttgttttg aacagtgaac att 33

<210> 75
 <211> 36
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic Primer

<400> 75
 tatgccggct actttggcaa gcttgaacat aaactc 36

<210> 76
 <211> 37
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic Primer

<400> 76
 ggcctcgagc taattcttgt tttgaacagt gaacatt 37

<210> 77
 <211> 28
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic Primer

 <400> 77
 atggccgaca aggtcctgaa ggagaaga 28

 <210> 78
 <211> 33
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic Primer

 <400> 78
 ttaatgtcct gggaagaggt agaaacatct tgt 33

 <210> 79
 <211> 26
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic Primer

 <400> 79
 tcaagccac aatctggaaa ttctca 26

 <210> 80
 <211> 26
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic Primer

 <400> 80
 ctggagagtc actgatcaac agttcc 26

 <210> 81
 <211> 36
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic Primer

 <400> 81
 acaaggatcc accatggccg acaaggatct gaaggg 36

 <210> 82
 <211> 39

<212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic Primer

 <400> 82
 cgcctctaga cctcaattgc caggggaagag atagaagta 39

<210> 83
 <211> 60
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic Primer

 <400> 83
 ctgcagtggg ggcgggtggcg gcggatctag aaacttgcca acccctactc catccccggg 60

<210> 84
 <211> 60
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic Primer

 <400> 84
 cccgggggatg gagtaggggt tggcaagttt ctagatccgc cgccaccgcc accactgcag 60

<210> 85
 <211> 28
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic Primer

 <400> 85
 atgcatactc agcagttggt catgcct 28

<210> 86
 <211> 25
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic Primer

 <400> 86
 tgcaggacac ggatgcccag ttgct 25

<210> 87
 <211> 37
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic Primer

 <400> 87
 acaggtacca tgcatacctca gcagttgggc atcgccct 37

 <210> 88
 <211> 25
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic Primer

 <400> 88
 ctaactgcag gacacggatg cccag 25

 <210> 89
 <211> 19
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic Primer

 <400> 89
 atgtgcccgc cgcgtggcc 19

 <210> 90
 <211> 27
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic Primer

 <400> 90
 ctaggaagca ttcagatagc tcatcat 27

 <210> 91
 <211> 39
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic Primer

<400> 91
 tatgaccg cg g gatgttcca gtgcctcaac cactcccaa 39

<210> 92
 <211> 41
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic Primer

<400> 92
 atgactgcgg cgcctagga agcattcaga tagctcatca t 41

<210> 93
 <211> 20
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic Primer

<400> 93
 ccatcctggc cctgctaagc 20

<210> 94
 <211> 22
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic Primer

<400> 94
 ccatctggta catcttcaag tc 22

<210> 95
 <211> 38
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic Primer

<400> 95
 aaaaaaccgc ggtatgttcc aatgtttcaa ccactccc 38

<210> 96
 <211> 51
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic Primer

 <400> 96
 gcggccgctc gagttaggaa gagttcaagt aggacatcat tctattgatg g 51

 <210> 97
 <211> 22
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic Primer

 <400> 97
 cttaaaggaa cagaaagaat cc 22

 <210> 98
 <211> 19
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic Primer

 <400> 98
 ggtattccca gctgacctc 19

 <210> 99
 <211> 37
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic Primer

 <400> 99
 cataggtacc atgcaccctc agcagttggt catctcc 37

 <210> 100
 <211> 29
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic Primer

 <400> 100
 atctaaatgc atgacacaga tgcccagtc 29

 <210> 101
 <211> 561

<212> DNA
 <213> Felis catus

<220>
 <221> CDS
 <222> (1)..(561)

<400> 101
 ggg atg ttc cag tgc ctc aac cac tcc caa acc ctg ctg cga gcc atc 48
 Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu Leu Arg Ala Ile
 1 5 10 15
 agc aac acg ctt cag aag gcc aga caa act cta gaa ttt tac tcc tgc 96
 Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys
 20 25 30
 act tcc gaa gag att gat cat gaa gat atc aca aaa gat aaa acc agc 144
 Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser
 35 40 45
 aca gtg gag gcc tgc tta cca ctg gaa tta acc atg aat gag agt tgc 192
 Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn Glu Ser Cys
 50 55 60
 ctg gct tcc aga gag atc tct ctg ata act aat ggg agt tgc ctg gcc 240
 Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala
 65 70 75 80
 tcc aga aag acc tct ttt atg acg acc ctg tgc ctt agc agt atc tat 288
 Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr
 85 90 95
 gag gac ttg aag atg tac cag gtg gag ttc aag gcc atg aat gca aag 336
 Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala Met Asn Ala Lys
 100 105 110
 ctg tta atg gat cct aaa agg cag atc ttt ctg gat caa aac atg ctg 384
 Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu
 115 120 125
 aca gct att gat gag ctg tta cag gcc ctg aat gtc aac agt gtg act 432
 Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val Asn Ser Val Thr
 130 135 140
 gtg cca cag aac tcc tcc ctg gaa gaa ccg gat ttt tat aaa act aaa 480
 Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys
 145 150 155 160
 atc aag ctc tgc ata ctt ctt cat gct ttc aga att cgt gca gtg acc 528
 Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr
 165 170 175
 atc aat aga atg atg agc tat ctg aat gct tcc 561
 Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser
 180 185

<210> 102
 <211> 187
 <212> PRT
 <213> Felis catus

<400> 102

Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu Leu Arg Ala Ile
 1 5 10 15

Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys
 20 25 30

Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser
 35 40 45

Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn Glu Ser Cys
 50 55 60

Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala
 65 70 75 80

Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr
 85 90 95

Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala Met Asn Ala Lys
 100 105 110

Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu
 115 120 125

Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val Asn Ser Val Thr
 130 135 140

Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys
 145 150 155 160

Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr
 165 170 175

Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser
 180 185

<210> 103

<211> 561
 <212> DNA
 <213> Felis catus

<400> 103
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 aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggttcttcca gggaggagtt 120
 ctgtggcaca gtcacactgt tgacattcag ggctgtaac agctcatcaa tagctgtcag 180
 catgttttga tccagaaaga tctgcctttt aggatccatt aacagctttg cattcatggc 240
 cttgaactcc acctggtaca tcttcaagtc ctcatagata ctgctaaggc acagggtcgt 300
 cataaaagag gtctttcttg aggccaggca actcccatta gttatcagag agatctctct 360
 ggaagccagg caactctcat tcatggttaa ttccagtggc aagcaggcct ccactgtgct 420
 gggttttatct tttgtgatat cttcatgac aatctcttcg gaagtgcagg agtaaaattc 480
 tagagtttgt ctggccttct gaagcgtggt gctgatggct cgcagcaggg tttgggagtg 540
 gttgaggcac tggaacatcc c 561

<210> 104
 <211> 1455
 <212> DNA
 <213> Canis familiaris

<220>
 <221> CDS
 <222> (232) .. (897)

<400> 104
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 agacagagag agaaagcaag ccggacaccg gagtcccgga aaagtccctg cgcgccctcg 120
 gcccaattata aaaatgtgac cccccgggtc ggccctccac cgccgcccctc ccctgccgcg 180
 tccgcagtcc gcgtccagcg cccgcggggg tccacgcagc gcccgcccag c atg tgc 237
 Met Cys
 1
 ccg ccg cgc ggc ctc ctc ctt gtg acc atc ctg gtc ctg cta agc cac 285
 Pro Pro Arg Gly Leu Leu Leu Val Thr Ile Leu Val Leu Leu Ser His
 5 10 15
 ctg gac cac ctt act tgg gcc agg agc ctc ccc aca gcc tca ccg agc 333
 Leu Asp His Leu Thr Trp Ala Arg Ser Leu Pro Thr Ala Ser Pro Ser
 20 25 30
 cca gga ata ttc cag tgc ctc aac cac tcc caa aac ctg ctg aga gcc 381
 Pro Gly Ile Phe Gln Cys Leu Asn His Ser Gln Asn Leu Leu Arg Ala

35	40	45	50	
gtc agc aac acg ctt cag aag gcc aga caa act cta gaa tta tat tcc				429
Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Leu Tyr Ser	55	60	65	
tgc act tcc gaa gag att gat cat gaa gat atc aca aag gat aaa acc				477
Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr	70	75	80	
agc aca gtg gag gcc tgc tta cca ctg gaa tta acc atg aat gag agt				525
Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn Glu Ser	85	90	95	
tgc ctg gct tcc aga gag atc tct ttg ata act aac ggg agt tgc ctg				573
Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser Cys Leu	100	105	110	
gcc tct gga aag gcc tct ttt atg acg gtc ctg tgc ctt agc agc atc				621
Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu Ser Ser Ile	115	120	125	130
tat gag gac ttg aag atg tac cag atg gaa ttc aag gcc atg aac gca				669
Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala Met Asn Ala	135	140	145	
aag ctt tta atg gat ccc aag agg cag atc ttt ctg gat caa aac atg				717
Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met	150	155	160	
ctg aca gct atc gat gag ctg tta cag gcc ctg aat ttc aac agt gtg				765
Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe Asn Ser Val	165	170	175	
act gtg cca cag aaa tcc tcc ctt gaa gag ccg gat ttt tat aaa act				813
Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr	180	185	190	
aaa atc aag ctc tgc ata ctt ctt cat gct ttc aga att cgt gcg gtg				861
Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val	195	200	205	210
acc atc gat aga atg atg agt tat ctg aat tct tcc taaaaagctg				907
Thr Ile Asp Arg Met Met Ser Tyr Leu Asn Ser Ser	215	220		
aggtctctct cgactttaaa gtcattccta taaaaatgtg aaccctaaaag aatttttcat				967
aagatagggg ttaagaacca gggaggggggt ggcttgacct ggtcctactt aagctagtag				1027
gataattctc atgcttggtt acattagttg ccactcaaat tttgaaagat gtgactgtta				1087
tatcccacac gatgcctttg accaagtata tttcacattt actatggata agttaagtgt				1147
tcgtgagcaa attgctaaag aggaaaaatg tcctcaccga acatgtttttt attttccctt				1207
taatagaaga gcaagacttt ataagctatt tctgtaccaa actgtttgtg gaaacaaaca				1267

ctcaagcata atttatttaa aaatacttat ttatataatt ttgtgttcat gaaagcatgt 1327
gaattaatth atatttatth atgttatatt tattaaagta tttattatca agtggatttg 1387
ggatatctta tgttctaaaa ataaaatgat tgagtagaaa aaaaaaaaaa aaaaaaaaaa 1447
aaaaaaaaa 1455

<210> 105
<211> 222
<212> PRT
<213> Canis familiaris

<400> 105

Met Cys Pro Pro Arg Gly Leu Leu Leu Val Thr Ile Leu Val Leu Leu
1 5 10 15

Ser His Leu Asp His Leu Thr Trp Ala Arg Ser Leu Pro Thr Ala Ser
20 25 30

Pro Ser Pro Gly Ile Phe Gln Cys Leu Asn His Ser Gln Asn Leu Leu
35 40 45

Arg Ala Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Leu
50 55 60

Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp
65 70 75 80

Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn
85 90 95

Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser
100 105 110

Cys Leu Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu Ser
115 120 125

Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala Met
130 135 140

Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln
145 150 155 160

Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe Asn
165 170 175

Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr
180 185 190

Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg
195 200 205

Ala Val Thr Ile Asp Arg Met Met Ser Tyr Leu Asn Ser Ser
210 215 220

<210> 106
<211> 1455
<212> DNA
<213> Canis familiaris

<400> 106
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attaattcac atgctttcat gaacacaaaa ttatataaat aagtattttt aaataaatta 180
tgcttgagtg tttgtttcta caaacagttt ggtacagaaa tagcttataa agtcttgctc 240
ttctattaaa gggaaaataa aaacatgttc ggtgaggaca tttttcctct ttagcaattt 300
gctcacgaac acttaactta tccatagtaa atgtgaaata tacttggtca aaggcatcgt 360
gtgggatata acagtcacat ctttcaaaat ttgagtggca actaatgtaa acaagcatga 420
gaattatcgt actagcttaa gtaggaccag gtcaagccac cccctccctg gttcttaacc 480
cctatcttat gaaaaattct tttgggttca catttttata ggaatgactt taaagtcgag 540
agagacctca gctttttagg aagaattcag ataactcatc attctatcga tggtcaccgc 600
acgaattctg aaagcatgaa gaagtatgca gagcttgatt ttagttttat aaaaatccgg 660
ctcttcaagg gaggatttct gtggcacagt cacactgttg aaattcaggg cctgtaacag 720
ctcatcgata gctgtcagca tgttttgata cagaaagatc tgcctcttgg gatccattaa 780
aagctttgcg ttcattggcct tgaattccat ctggtacatc ttcaagtcct catagatgct 840
gctaaggcac aggaccgtca taaaagaggc ctttccagag gccaggcaac tcccgttagt 900
tatcaaagag atctctcttg aagccaggca actctcattc atggttaatt ccagtggtaa 960
gcaggcctcc actgtgctgg ttttatecct tgtgatattc tcatgatcaa tctcttcgga 1020
agtgcaggaa tataattcta gagtttgtct ggccttctga agcgtgttgc tgacggctct 1080

cagcaggttt tgggagtggg tgaggcactg gaatattcct gggctcgggtg aggctgtggg 1140
gaggctcctg gcccaagtaa ggtgggtccag gtggcttagc aggaccagga tggtcacaag 1200
gaggaggccg cgcggcgggc acatgctggg cgggcgctgc gtggaccccg gcgggcgctg 1260
gacgcggact gcggacgcgg caggggaggg cggcgggtggg aggccgaccc ggggggtcac 1320
atttttataa ttggcccagag gcgcgccagg actttcccgg gactccgggtg tccggcttgc 1380
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ggtttgccctc gtgcc 1455

<210> 107
<211> 2267
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (154)..(1140)

<400> 107
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ggagtagggg atataagctc cagtagcagt agcagcagca gcaggagact ccgtttcaga 120
cccagggaaac cttgcagcct ggccagaagc aag atg cat cct cag cag ttg gtc 174
Met His Pro Gln Gln Leu Val
1 5
atc tcc tgg ttt tcc ctc gtt ttg ctg gcg tct ccc ctc atg gcc ata 222
Ile Ser Trp Phe Ser Leu Val Leu Leu Ala Ser Pro Leu Met Ala Ile
10 15 20
tgg gaa ctg gag aaa gat gtt tat gtt gta gag ttg gac tgg cac cct 270
Trp Glu Leu Glu Lys Asp Val Tyr Val Val Glu Leu Asp Trp His Pro
25 30 35
gat gcc ccc gga gaa atg gtg gtc ctc acc tgc cat acc cct gaa gaa 318
Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys His Thr Pro Glu Glu
40 45 50 55
gat gac atc act tgg acc tca gcg cag agc agt gaa gtc cta ggt tct 366
Asp Asp Ile Thr Trp Thr Ser Ala Gln Ser Ser Glu Val Leu Gly Ser
60 65 70
ggt aaa act ctg acc atc caa gtc aaa gaa ttt gga gat gct ggc cag 414
Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly Gln
75 80 85
tat acc tgc cat aaa gga ggc aag gtt ctg agc cgc tca ctc ctg ttg 462
Tyr Thr Cys His Lys Gly Gly Lys Val Leu Ser Arg Ser Leu Leu Leu

90	95	100	
att cac aaa aaa gaa gat gga att tgg tcc act gat atc tta aag gaa Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys Glu 105 110 115			510
cag aaa gaa tcc aaa aat aag atc ttt ctg aaa tgt gag gca aag aat Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys Asn 120 125 130 135			558
tat tct gga cgt ttc aca tgc tgg tgg ctg acg gca atc agt act gat Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr Asp 140 145 150			606
ttg aaa ttc agt gtc aaa agt agc aga ggc ttc tct gac ccc caa ggg Leu Lys Phe Ser Val Lys Ser Ser Arg Gly Phe Ser Asp Pro Gln Gly 155 160 165			654
gtg aca tgt gga gca gtg aca ctt tca gca gag agg gtc aga gtg gac Val Thr Cys Gly Ala Val Thr Leu Ser Ala Glu Arg Val Arg Val Asp 170 175 180			702
aac agg gat tat aag aag tac aca gtg gag tgt cag gag ggc agt gcc Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser Ala 185 190 195			750
tgc ccc tct gcc gag gag agc cta ccc atc gag gtc gtg gtg gat gct Cys Pro Ser Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp Ala 200 205 210 215			798
att cac aag ctc aag tat gaa aac tac acc agc agc ttc ttc atc aga Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile Arg 220 225 230			846
gac atc atc aaa cca gac cca ccc aca aac ctg cag ctg aag cca ttg Asp Ile Ile Lys Pro Asp Pro Pro Thr Asn Leu Gln Leu Lys Pro Leu 235 240 245			894
aaa aat tct cgg cac gtg gag gtc agc tgg gaa tac ccc gac acc tgg Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr Trp 250 255 260			942
agc acc cca cat tcc tac ttc tcc ctg aca ttt tgc ata cag gcc cag Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Ile Gln Ala Gln 265 270 275			990
ggc aag aac aat aga gaa aag aaa gat aga ctc tgc gtg gac aag acc Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Cys Val Asp Lys Thr 280 285 290 295			1038
tca gcc aag gtc gtg tgc cac aag gat gcc aag atc cgc gtg caa gcc Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln Ala 300 305 310			1086
cga gac cgc tac tat agt tca tcc tgg agc gac tgg gca tct gtg tcc Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asp Trp Ala Ser Val Ser 315 320 325			1134

tgc agt taggttccac ccccaggatg aatcttggag ggaaagtgga agatattatg 1190
Cys Ser

caaaattttc taaggacaca ttgaagaggc tccaaaagtt attttctgcc taattttctt 1250
tttgtaaagg gtcattattg tgtcttcgca atatttttta catttaaag ccaaagcccc 1310
actgaaacaa tcagctactt tatttataga ttttcagcta gcaggctgcc actgacctta 1370
atgctattta aatattttaag taatttatgt atttattaat ttattgttat tgaacacttg 1430
tgtgccaaga tatattgtat gtttcatacc ctcaggacct gatctgtaag gaataggccc 1490
tattatgcaa aatgtgaatt tatgtgttat ttatactgac aacttttcaa gcaagaatgt 1550
atcattttta tgacaaccag tgagcacaca atattatgat gccagcacca taatatattt 1610
gtgatggatg ggaacacaga ggtagttaaa tagagacatg gagacacgaa tccatttgag 1670
aagtttctgg agacggagat gttagatcct gtatccataa agacttcctt gcggtggtgt 1730
tgataaagca attcagggcc acttgcattt ttaagcaagt ttagtttttg gatgcctgaa 1790
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gaagtaaaaa ggtcttatga tccaagaggg agaaccaaca tggccaagca caaaaaattg 1970
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tggtcaagaa ttgcttactg gacagcgcaa gtgaacctga ctggtggatg tgaccagaaa 2090
gtgccaatcg ctgaggtgct acttttaagt aatgaatgtg ctttctgtaa agtgatttca 2150
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tcttgtttgc aataataaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 2267

<210> 108

<211> 329

<212> PRT

<213> Canis familiaris

<400> 108

Met His Pro Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Leu Leu
1 5 10 15

Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asp Val Tyr Val
20 25 30

Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
 35 40 45
 Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln
 50 55 60
 Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
 65 70 75 80
 Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val
 85 90 95
 Leu Ser Arg Ser Leu Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
 100 105 110
 Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
 115 120 125
 Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
 130 135 140
 Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg
 145 150 155 160
 Gly Phe Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser
 165 170 175
 Ala Glu Arg Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
 180 185 190
 Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro
 195 200 205
 Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
 210 215 220
 Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr
 225 230 235 240
 Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
 245 250 255
 Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu

260	265	270
Thr Phe Cys Ile Gln Ala Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp		
275	280	285
Arg Leu Cys Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp		
290	295	300
Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp		
305	310	315
		320
Ser Asp Trp Ala Ser Val Ser Cys Ser		
	325	

<210> 109
 <211> 2267
 <212> DNA
 <213> Canis familiaris

<400> 109
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 aatcacttta cagaaagcac attcattact taaaagtagc acctcagcga ttggcacttt 180
 ctgggtcacat ccaccagtca ggttcacttg cgctgtccag taagcaattc ttgaccattt 240
 tctttgcatc catgtgcttt ttttgcttgg ctattaagga gcagctggaa attctgacaa 300
 ttttttgtgc ttggccatgt tggttctccc tcttgatca taagacctt ttacttccag 360
 acacttacag tgtccctggg tcaactctcca atgacttaca gatagatggg gatggggact 420
 ggcaagggtg ctgaagctga atctcaattt gagttatttg tctcaggtct ttctaaattc 480
 aggcatccaa aaactaaact tgcttaaaaa tgcaagtggc cctgaattgc tttatcaaca 540
 ccaccgcaag gaagtcttta tggatacagg atctaacatc tccgtctcca gaaacttctc 600
 aaatggattc gtgtctccat gtctctattt aactacctct gtgttcccat ccatcacaaa 660
 tatattatgg tgctggcatc ataattttgt gtgtcactg gttgtcataa aaatgatata 720
 ttcttgcttg aaaagttgtc agtataaata acacataaat tcacattttg cataataggg 780
 cctattcctt acagatcagg tcctgagggg atgaaacata caatatatct tggcacacaa 840
 gtgttcaata acaataaatt aataaataca taaattactt aaatatttaa atagcattaa 900
 ggtcagtggc agcctgctag ctgaaaatct ataaataaag tagctgattg tttcagtggg 960

catttggcat ttaaagttaa aaaatattgc gaagacacaa taatgaccct ttacaaaaag	1020
aaaattagggc agaaaataac ttttggagcc ttttcaatgt gtccttagaa aattttgcat	1080
aatatcttcc actttccctc caagattcat cctgggggtg gaacctaaact gcaggacaca	1140
gatgcccagt cgctccagga tgaactatag tagcgggtctc gggcttgac gcggatcttg	1200
gcacccctgt ggcacacgac cttggctgag gtcttgtcca cgcagagtct atctttcttt	1260
tctctattgt tcttgccctg ggctgtatg caaaatgtca gggagaagta ggaatgtggg	1320
gtgctccagg tgtcggggta ttcccagctg acctccagct gccgagaatt tttcaatggc	1380
ttcagctgca ggtttgtggg tgggtctggt ttgatgatgt ctctgatgaa gaagctgctg	1440
gtgtagtttt catacttgag cttgtgaata gcaccacca cgacctgat gggtaggctc	1500
tcctcggcag aggggcaggc actgccctcc tgacactcca ctgtgtactt cttataatcc	1560
ctgttgtcca ctctgaccct ctctgctgaa agtgtcactg ctccacatgt cacccttgg	1620
gggtcagaga agcctctgct acttttgaca ctgaatttca aatcagtact gattgccgtc	1680
agccaccagc atgtgaaacg tccagaataa ttctttgcct cacatttcag aaagatctta	1740
tttttggatt ctttctgttc ctttaagata tcagtggacc aaattccatc ttcttttttg	1800
tgaatcaaca ggagtgagcg gctcagaacc ttgcctcctt tatggcaggt atactggcca	1860
gcacctccaa attctttgac ttggatggtc agagttttac cagaacctag gacttcactg	1920
ctctgcgctg aggtccaagt gatgtcatct tcttcagggg tatggcaggt gaggaccacc	1980
atttctccgg gggcatcagg gtgccagtc aactctacaa cataaacatc tttctccagt	2040
tcccatatgg ccatgagggg agacgccagc aaaacgaggg aaaaccagga gatgaccaac	2100
tgctgaggat gcaccttgct tctggccagg ctgcaaggtt ccctgggtct gaaacggagt	2160
ctctgctgc tgctgctact gctactggag cttatatacc ctactcctac cgagcttttg	2220
gatggaaact taaactagaa actgacttgt ccaagttgcc tcgtgcc	2267

<210> 110
 <211> 7
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Linker

<400> 110

Gly Gly Gly Gly Gly Gly Ser
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<210> 111
<211> 10
<212> PRT
<213> Felis catus

<400> 111

Arg	Asn	Leu	Pro	Thr	Pro	Thr	Pro	Ser	Pro
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